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173 GIGGIGACGCIACIGCTGCTGATCGCTGCCACTTTCCTGTGGAACCTGCTGGTTCCG 232
113 ACCCCAACGAGGCGCCGTCCTGCCGGGCCGAGGGCCGCCTTCTCTGTCTTCACGGTCCTG
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                                                                                                                                                             Sequence 8, Application US/08356405
Sequence 8, Application US/08356405
Patent No. 5807691
APPLICANT: Amlaiky, No. 5807691rdine
APPLICANT: Hen, Boschert, Ursula
APPLICANT: Hen, Boschert, Ursula
APPLICANT: Hen, Polypeptides Having Serotonin Receptor
TITLE OF INVENTION: Polypeptides Having Serotonin Receptor
TITLE OF INVENTION: Activity (5HT5A), Nucleic Acids Coding for
TITLE OF INVENTION: Polypeptides and Uses Thereof
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
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Pred. No. 8.6e-94;
0; Mismatches 284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR93/00650
FILING DATE: 29-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/08081
FILING DATE: 01-JUL-1992
ATTORNEY/AGENT INFORMATION:
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ER: EX92004-US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                      SEE: Rhone-Poulenc Rorer: 500 Arcola Road, 3C43
Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION TELEPHONE: (610) 454-3839
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ilarity 70.0%;
Conservative
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Smith, Julie K
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA ORIGINAL SOURCE:
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SOFTWARE: PatentI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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                                                                                                                                                 RESULT 2
US-08-356-405-8
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Matches
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

7, 2004, 15:17:31 ; Search time 109 Seconds (without alignments) 5865.169 Million cell updates/sec September Run on:

US-09-976-782-15 1152

Perfect score: Sequence:

1 cgccatggaggccgctagcc.....aagcagagatgaacacaggg 1152

Scoring table:

682709 seqs, 277475446 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

1365418

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

lssued_patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/pcTus_comB.seq:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	US-08-031-538-1	US-08-356-405-8	US-08-356-405-1	US-08-031-538-3	-016-	-016-434-1	US-09-016-434-1197	US-08-475-742-15	-08-261-293-1	-594-6	01-2	-351-473B	US-08-334-698-3	US-08-228-932-3	Ö	Ö	-061	-244-354-	6	US-09-444-783-3	US-09-688-415-3	US-09-016-434-1402	3-3	PCT-US95-04203-3	US-09-032-742-6	-08-087-772A	US-07-916-901-1
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ф	Query Match	6	42.0	'n	36.1		8.3	8.2	8.1	8.1	•	•	7.8	•	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	•		7.7	7.7
	Score	729.8	484.4	424.6	4	104.4	95.2	94	93	93	69	91.2	89.8			88.8	88.8	88.8		88.8			88.8		-		88.2	
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US-09-016-434-1184	118-08-450-962-1	1 400 001 00 00	US-08-848-631-1	US-09-016-434-1243	US-08-722-001-26	116-00-120-001	17-TOO-771-00-50	US-08-722-001-11	US-08-334-698-5	TIS=08-228-18	0 300 037 00 00	US-08-468-939-5	US-08-406-855A-5	11S-08-722-190-E	C-077 331 00 00	US-08-244-354-5	US-09-206-899-5	TIS-09-444-783-E	0.00/. 111 00.00	US-09-688-415-5	US-09-444-783-5	The second second second	PCI-0595-04203-5
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ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: Sutcliffe, J Gregor
APPLICANT: Lovenberg, Timothy W
TITLE OF INVENTION: HUMAN SEROTONIN RECEPTORS, DNA ENCODING
TITLE OF INVENTION: THE RECEPTORS, AND USES THEREOF
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Soribps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5968817th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/031,538
FILING DATE: 19930315
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.4%; Score 729.8; DB 2; 79.6%; Pred. No. 1.3e-145; tive 0; Mismatches 207;
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                                                 Sequence 1, Application US/08031538 Patent No. 5968817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRS:
TELECOMMUNICATION INFORMATION:
TELEFROME 619-554-2937
TELEFRAX: 619-554-2937
TELEFRAX: 619-554-2937
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 2226 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 79.6
Matches 911; Conservative
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USA
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US-08-031-538-1
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RESULT 1
US-08-031-538-1
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Gaps

27;

Length 2226; Indels ന

WO200210387-A2 07-FEB-2002 Peptide Protein Domain Domain KANANA KA

pick's disease, Huntington's disease, Parkinson's disease, hypertension, atherosclerosis, myocardial infarction, gastritis, cirrhosis, cytostatic, osteoporosis, Crohn's disease, acquired immunodeficiency syndrome, ALDS, anaemia, asthma; rheumatoid arthritis, diabetes; obesity, drug screening, transgenic animal, allergy, gene therapy, hepatotropic, anticonvulsant, nootropic, neuroprotective, cardiant, immunosuppressive; anorectic; virucide, receptor.

Homo sapiens

/note= "Transmembrane domain" /label= Human_mature_GCREC-15 298. .316 /note= "Transmembrane domain" 1. .65 /label= Signal_peptide Location/Qualifiers , 68

2000US-0221478P. 2000US-0223268P. 2000US-0227054P. 2000US-0231121P. 2000US-0232243P. 2000US-0235146P. 25-JUL-2001; 2001WO-US023433 08-SEP-2000; 13-SEP-2000; 15-SEP-2000; 03-AUG-2000; 21-AUG-2000; 22-SEP-2000;

(INCY-) INCYTE GENOMICS INC.

Thornton M, Patterson C, Lal P, Burford N, Yue H, Gandhi AR; Elliot VS, Ramkumar J, Baughn MR, Kallick DA, Walia NK, Hafalia AJA; Yao MG, Lu Y, Tribouley CM, Policky JL, Kearney L, Graul RC; Warren BA, Lee EA, Ding L;

WPI; 2002-188744/24. N-PSDB; AAD29681. New human G-protein coupled receptor polypeptide for diagnosis, prevention and treatment of cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune/inflammatory, and metabolic disorders

Claim 1; Page 133-134; 150pp; English.

The invention features to mover numan verponent coupled receptors (ucket) and their encoding polymucleotides. GCREC is useful as an immunogen for preparing monoclonal and polyclonal antibodies. GCREC is useful for diagnosing, treating and preventing a cell proliferative disorder (e.g., cheating and preventing a cell proliferative disorder (e.g., cheating and preventing a cell proliferative disorder (e.g., proliferative disorder). Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's CG disease), a cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infarction), gastrointestinal disorder (e.g., gastritis, cirrhosis, Crohn's disease), an autoimmune/ inflammatory disorder (e.g., cirrhosis, crohn's disease), an autoimmune/ inflammatory disorder (e.g., cirrhosis, asthma, crohniques, and to analyse the proteome of a tissue or cell transpening techniques, and to analyse the proteome of a tissue or cell type. GCREC is useful for creating knockin humanised animals or transpenic animals to model human diseases, in somatic or germline gene conterpray, to generate a transcript image of a tissue or cell type, for therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromonal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as the proteor or probes for mapping naturally occurring genomic sequences. CG TREC is useful in Southern or northern analysis, dot blot or other communication multiformat enzyme linked immunosorbant (ELISA)-like assays, and in The invention relates to novel human G-protein coupled receptors (GCREC)

888	microarrays utilising fluids or tissues from patients to detect altered GCREC expression. The present sequence is human GCREC-15
S S	Sequence 370 AA;
Aligni Pred. Score Percei Best l Query	gnment Scores: 1.86e-136 Length: 370 d. No.: 1861.50 Matches: 370 cent Similarity: 97.63\$ Conservative: 0 iry Match: 86.42\$ Indels: 9 Gaps: 3
US-C	09-976-782-15 (1-1152) x AAE18654 (1-370)
ò	IGGAGGCCGTAGCCTTTCAGTGGCCACCGCCGCGGCGTTGCCCTTGCCCTGGG
qq	
λο dd	65 ACCAGCAGCGGACCCGAAGCCCGAGAGGATACTCGGTTCGACCCCGAGCGGC 124 [
ò	5 GCCGTCCTGCCCGGCCCGAGGCCCCTTCTCTGTCTTCACGGTCCTGGTGACGCTG 1
qq	
7	5 CTAGTGCTGATCGCTGCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCACCATCCCG 2
QC	JValLeuLeuileAlaAlaThrPheLeuTrpAsnLeuLeuValProValThrilePr
ò	245 CGGGTCCGTGCCTTCCACCGCGCGCATAACTTGGTGGCCCTCGACGGCCGTCTCGGAC 304
qq	yyalArgAlaPheHisArgValProHisAsnLeuValAlaSerThrAlaValSe
ò	305 GAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCCAGTGAGCTGTCGACCGGCGA 364
QC	euvalalaalaLeualaMetProProSerLeualaSerGluLeuSerThrGly
ò	365 CGTCGGCTGCTGGGCCGGGAGCCTGTGCGAGTGTGGATCCCTTCGACGCCGGAGCCTGT 424
qq	rgbeuLeuGlyArgSerLeuCysHisValTrpIleSerPheAspAl
δλ	25 CTGTGCTGCCCCGCCGCCTCGGGAACGTGGCGGCCATCGCCCTGGGCCGCGACGAGGCC 48
පි	uCysCysProAlaGlyLeuGlyAsnValAlaAlaIleAlaLeuGlyArgAspGlyAl
ò	S ATCACACGCACCTGCAGCACACCGCACCCGCACCCGCGCCCTCGTTGCTCATGATC 5
අු	eThrArgHisLeuGlnHisThrLeuArgThrArgSerArgAlaSerLeuLeuMetIl
δ	45 GCGCTCGCCCGGGTGCCGTCGGCGCTCATCGCCCCTCGCGCCCCTTGCTTTTGGCCGGGGC 60
වු	6 AlaLeuAlaArgValProSerAlaLeuIleAlaLeuAlaProLeuLeuPheGlyArgGl
ð :	05 GAGGTGTGCGACGCTCGGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCCTATGCCGCC 66
qq	alCysAspAlaArgLeuGlnArgCysGlnValSerArgGluProSerTyrAlaAl
ò	CTCCACCCCCGCGCGCCTTCCACCTGCCGCTTGGCGTGCTGCCGTTTGTCTACCG
QQ	erThrArgGlyAlaPheHisLeuProLeuGlyValValProPheValTyrArg
ò	GAGGCGCCAAGTTTCGTTTCGGCCGCCGCCGGAGAGCTGT
g	eTyrGluAlaAlaLysPheArgPheGlyArgArgArgArgAlaValLeuProLeuPr
à	CAGGTGAGGTCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGT
Op	aThrMetGlnVallysGluAlaProAspGluAlaGluValValPh
ò	845 ACGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGGGAGCAG 904

us-09-976-782-15.n2p.rag

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The present invention provides the protein and coding sequences pf novel human G-protein coupled receptors, designated NOV1, NOV2, NOV3, NOV4, NOV5a, NOV5b, NOV7b, NOV8b, NOV9b, NOV9b, NOV9b, NOV7b, NOV7b, NOV9b, NOV9b, NOV7b, NOV7b, NOV7b, NOV5b, NOV5b,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          605 GAGGTGTGCGACGCTCGGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCCTATGCCGCC 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 ThrserSer-----GlyThrProSerProArgGlyTleLeuGlySerThrProSerGly 38
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            New G protein-coupled receptor related polypeptides and polynucleotides for diagnosis, prevention and treatment of metabolic, neurodegenerative, retinal, immune, hematopoietic disorders, diabetes, obesity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluValCysAspAlaArgLeuGlnArgCysGlnValSerArgGluProSerTyrAlaAla
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97.63%
86.37%
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                                      AAGGAGAGGCGAGCCATGATGGTGGGGAATTCTGATTGGCGTGTTTGTGCTGTGCTGG 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; NOV5a; metabolic disorder; neurodegenerative disorder; immune disorder; haematopoietic disorder; developmental disease; cancer; retinal disease; feeding disorder; vaccine; infection; gene therapy; neurological disorder; psychotic disorder; G-protein coupled receptor; cytostatic; antidiabetic; virucide; neuroprotective; nootropic; antiagepressant; antimiganie, anticonvulsant; neuroleptic; antiasthmatic; antiatheroscierotic; antibacterial; norectic; antiarthritic; antipsoriatic; antiatheroscierotic; antibacterial; fungicide; antibacterial; tytoroscade; antiulcer; hyperensive, hypotensive; serotonin receptor; chromosome 2.
                                                                                                                                                                                                                                                                        ACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAGA 1141
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                                                             ThrAlaHisCysLysAlaThrValSerPheGlnValSerGlyAspSerTrpArgGluGln
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Liu X, Patturajan M, Gusev
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/label= signal_peptide
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Shimkets RA,
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immune disorder; haematopoietic disorder; developmental disease; cancer; retinal disease; feeding disorder; vaccine; infection; gene therapy; neurological disorder; psychotic disorder; G-protein compled receptor; cytostatic; antidiabetic; virucide; neuroprotective; nootropic; analgesic; antidepressant; antimigraine; anticonvulsant; neuroleptic; antidepressant; antimiflammatory; anorectic; antiarthritic; antipsoriaric; antiatherosclerotic; antibacterial; fungicide; osteopathic; protozoacide; antiulcer; hypertensive; hypotensive; antimitier, antimitier, one antimitier of the control of 
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Patturajan M, Gusev VY;
                                                                                                                                                                                                Human; NOV5b; metabolic disorder; neurodegenerative disorder;
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10-APR-2000;
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Shimkets RA,
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29-MAR-2001;
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RESULT 3
ABA01985
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New G protein-coupled receptor related polypeptides and polymucleotides for diagnosis, prevention and treatment of metabolic, neurodegenerative, retinal, immune, hematopoietic disorders, diabetes, obesity and

2001-626379/72.

P-PSDB; AAM47212

The present invention provides the protein and coding sequences of novel human G-protein coupled receptors, designated NoV1, NoV2, NoV3, NOV4,

Claim 8; Page 46; 194pp; English.

infections,

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NOV5a, NOV5b, NOV6a, NOV6b, NOV7, NOV8a, NOV8b, NOV9 and NOV10. These can be used in the treatment of NOVX related diseases, including cancer, metabolic, neurodegenerative, immune, haematopoietic, devalopmental, retinal, feeding, neurological and psychotic diseases and disorders and infections. The present sequence is the NOV5b coding sequence, the gene for which is found on chromosome 2. The NOV5b protein shares homology
                                                                                                                                                                                                                                                                                                                                                                   180
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                                                                                                                                                                    Length 1150;
                                                                                                                                  Sequence 1150 BP; 178 A; 388 C; 355 G; 229 T; 0 U; 0 Other;
                                                                                                                                                                   DB 4;
                                                                                                                                                               Score 1064.8; DB 4;
Pred. No. 5.6e-221;
0; Mismatches 2;
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                                                                                                                                                                                Best_Local Similarity 97.5
Matches 1123; Conservative
                                                                                                with serotonin receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences pf novel human G-protein coupled receptors, designated NOV1, NOV2, NOV3, NOV4, NOV5a, NOV5b, Nov5b,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New G protein-coupled receptor related polypeptides and polynucleotides for diagnosis, prevention and treatment of metabolic, neurodegenerative, retinal, immune, hematopoietic disorders, diabetes, obesity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ceccangoageccecnadecinicagioseccacecececeriocentecenadadec
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ajan M, Gusev VY;
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Pred. No. 1.1e-221;
0; Mismatches 0; Indels 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 177 A; 388 C; 355 G; 230 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patturajan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Taupier RJ,
                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Page 42; 194pp; English.
serotonin receptor; chromosome 2;
                                                                                                                                          "NOV5a"
                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0195088P
2000US-0195792P
2000US-019656E
2000US-0197081P
2000US-0197087P
2000US-0197087P
200UUS-00823187
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Best Local Similarity 97.7%;
Matches 1125; Conservative
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13-APR-2000; 2
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Shimkets RA,
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US-08-356-405-1
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Sequence 1, Application US/08356405 Patent No. 5807691 GENERAL INFORMATION:

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APPLICANT: Amlaiky, No. 5807691rdine
APPLICANT: Boschert, Ursula
APPLICANT: Boschert, Ursula
APPLICANT: How, Rene
APPLICANT: How, Rene
TITLE OF INVENTION: Polypeptides Having Serotonin Receptor
TITLE OF INVENTION: Activity (5HT5A), Nucleic Acids Coding for These
TITLE OF INVENTION: Polypeptides and Uses Thereof
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,405
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Pred. No. 4.1e-81;
0; Mismatches 309;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR93/00650
FILING DATE: 29-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/08081
FILING DATE: 01-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Smith, Julie K
REGISTRATION NUMBER: 38,619
REPERNCE/DOCKET NUMBER: EX92004-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)454-3839
TELEFAX: (610)454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: Rhone-Poulenc Rorer Inc.: 500 Arcola Road, 3C43
Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 36.9%;
Best Local Similarity 67.3%;
Matches 684; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1686 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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813 AGGAAGCACCTGATGAGGTGTGTTTCACGGCACATTGCAAAGCAACGTGTCT 872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 416; DB 2; Length 21
Pred. No. 2.8e-79;
0; Mismatches 305; Indels
                                                                                                                                                                                      34,163
R: TSR5099P
                                US/08/031,538
                                                                                                                                               ALIONALIA PARATANANA BARBER BARGATRAN NUMBER: 34,163
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRS
TELEPONE: 619-554-2937
TELEPAK: 619-554-6312
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2155 DASE PAIS
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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66.8%;
                                                                                                                           ATTORNEY/AGENT INFORMATION:
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hes 663; Conservative
CURRENT APPLICATION DATA:
                                                          19930315
                             APPLICATION NUMBER:
FILING DATE: 199303:
CLASSIFICATION: 800
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Matches
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      487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sutcliffe, J Gregor
APPLICANT: Elander, Mark B
APPLICANT: Lovenberg, Timothy W
TITLE OF INVENTION: HUMAN SEROTONIN RECEPTORS, DNA F
TITLE OF INVENTION: THE RECEPTORS, AND USES THEREOF
ONRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08031538 Patent No. 5968817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92037
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MEDIUM TYPE: Floppy disk
COMPUTER: Elappy disk
COMPUTER: Elap PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
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Sequence 1077, Application US/09016434

Patent No. 650038

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECT:
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 13174 PORTER DRIVE
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Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
ITILE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 104.4; DB 4;
Pred. No. 2e-13;
0; Mismatches 306;
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STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PA-0002 US
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1256:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 49.4%;
Matches 313; Conservative
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APPLICATION NUMBER: US
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Pred. No. 1.9e-11;
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NAME: Zeller, Karen J.
REGISTRATION UNDHER: 37,071
REFERENCE/DOCKET NUMBER: PA-00
TELECOMMUNICATION INFORMATION:
TELEFRAM: (650) 855-0555
TELEFRAM: (650) 855-0556
INFORMATION FOR SEQ ID NO: 1077:
SEQUENCE CHARACTERISTICS:
LENGTH: 1994 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-09-016-434-1077
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834 AAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCT 893
                                                                                                                                                                                                                    1240 AddacaGCAGGAAGGCCCTGAAGGCCAGCCTGACGTGGGCATCTGGGCATGTTCT
                                                                                                                                                                                                                                                                                               TGCTGTGCTGGATCCCCTTCTTCCTGACGGAACTCATCAGCCCACTCTGTGCCTGCAGCC
                                                                                                                                                                                                                                                                                                                                                                   1300 rrgigaccriccricrirrirgiggccaacarachegeccaggcgrgrgcaacricri
                                                                                                                                                                                                                                                                                                                                                                                                                                           1360 ccccaggccrcrrcga---rgrccrcacarggcrgcrracraracagcaccargaacc
                                                                                                                                               GGCGGGAGCAGAAGAAGAGGAGCAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1197, Application US/09016434

Ratent No. 6500338
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Janice Au-Young
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAX GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
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1301 TCTACACCACCTTCAACATCGAGTTCCGCAAGGCCTTCATGAAGATCTT 1349
                                                                                                                                                            Sequence 15, Application US/08261293

Patent No. 6486310
GENERAL INFORMATION:
APPLICANT: O'Malley, Karen L.
APPLICANT: Todd, Richard D.
TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: 1...2428
OTHER INFORMATION: /note= "Rat d2 receptor sequence"
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Albert, P.
Salon, J.
Christie, M.
Machida, C. A.
Neve, K. A.
C. Civell, O.
Cloning and expression of a rat D2 dopamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; RELEVANT RESIDUES IN SEQ ID NO: 15: FROM 1 TO 2428
US-08-261-293-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachstree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,284
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: WU 102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6524
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/014,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Rattus norvegicus
TISSUE TYPE: Cardiac Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bunzow, J. R.
Van Tol, H. H.M.
Grandy, D. K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2428 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
EDNESS: single
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          783-787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1988
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                                                                                                                                  US-08-261-293-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
                                                                                                         RESULT 9
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                                                                                                                                                                                                                                                                                    1019
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                                                                                                                                                                                         1430 AGCAGAAGGAGAAGAAAGCCACTCAGATGCTCGCCATTGTTCTCGGCGTGTTCATCATCT 1489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1181 GCTGGCTGCCTTCTTCATCAGGCACATCCTGAATATACACTGTGATTGCAACATCCCAC
                                                                                                                                          900 AGCAGAAGGAGAGGCGAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGT
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                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1080 TITACACAGCITITAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTT 1129
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APPLICANT: O'Malley, Karen L
APPLICANT: O'Malley, Karen L
APPLICANT: O'Malley, Karen L
APPLICANT: Todd, Richard D
TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4 Receptor FILE REFERENCE: WU 102 CON DIV
CURRENT APPLICATION NUMBER: US/08/475,742
CURRENT FILING DATE: 1994-06-07
EARLIER APPLICATION NUMBER: US 08/261,293
EARLIER FILING DATE: 1994-06-16
EARLIER PILING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 16
   Length 1756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Franciscons | 
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Score 94; DB 4; Length 175 Pred. No. 3.4e-11; 0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08475742 Patent No. 6121015
Query Match
Best Local Similarity 63.0%;
Matches 145; Conservative
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SEQ ID NO 15
LENGTH: 2428
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ORGANISM: CDNA
FEATURE:
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GCCGCTTGGCGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCCAAGTTTCGTTT 750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATCGCCCTCGCCCCCTGCTCTTTGGCCGGGGGGGGGTGTGCGGACGCTCGGCTCCAGCG 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATCTCCATCGGCCTCTCCTTGGGTGGAAGGAGCCGGCACCCAACGAT---GACAAGGA 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCGGCCATCGCCCTGGGCCGCGA---CGGGGCCATCACACGCCACCTGCAGCACACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             476 GGTCACCCGGAGGAAGGCCATCTTGGCCCTGCTC---AGTGTCTGGGTCTTGTCCACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                                                        TITLE OF INVENTION: ALPHAIC ADRENERGIC RECEPTOR ANTAGONISTS NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                     Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 91.2; DB 1;
Pred. No. 1.3e-10;
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC CODS/MS-DOS
SOFTWATE: Patentin Release #1.0,
                                                                                                                                                                                                New Jersey
: United States of America
                                                                                                                                                                                                                                                                                                                                                                          US/08/722,001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMUNICATION INFORMATION:
TELEPHONE: (908) 594-3462
TELEPHONE: (908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         08/229,276
              Nerenberg, Jennie B.
Lee, Hee-Yoon
Bell, Ian M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                    ADDRESSEE: Merck & Co., Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34,087
                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: APPOLITINA, MARY A.
REGISTRATION NUMBER: 34,08
                                                                                                                                                       126 Lincoln Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 138825
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (900)...
(908)594-4720
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APPLICATION NUMBER: US
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Huff, Joel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
SDNESS: both
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                                                                                                                                                                          CITY: Rahway
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STRANDEDNESS
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Matches 383;
                APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT PILING DATE: 2001-10-12
PRIOR PILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGram
SEQ ID NO 629
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                  Score 93; DB 4; Length 2428; Pred. No. 5.8e-11;
                                                          85; Indels
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COTHER INFORMATION: Incyte ID No. 6673549 336435.2
US-09-976-594-629
                                                          0; Mismatches
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Patent No. 5760054
GENERAL INFORMATION:
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                    8.1%;
                                                          Matches 144; Conservative
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ORGANISM: Homo sapiens
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US-08-722-001-24
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us-09-976-782-15.rni

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642 GCCGGGAACCCTCCTATGCCGCCT--
             MOLECULE TYPE: DNA (genomic)
                                                    Query Match
Best Local Similarity 48.6%;
Matches 460; Conservative
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US-08-351-473B-7
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                                                                                                                                                                                                            CGGAACTCATCAGCCCACTCTGTGCCTGCAGCCTGCCCCC---CATCTGGAAAAGCATAT 1037
                                                                                                                                                                                                                                      946 CTCTACCGCTTGGCTCCTTGTTCTCCACCCTGAAGCCCCCGACGCCGTGTTCAAGGTGG 1005
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811 AAAGGAAGCACCTGATGAGGCTGAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTC
                                                                     768 --AGGATCCATTCCAAGAACTTTCACGAGGACACCCTTAGCAGTACCAAGGCCAAGGGCC
                                                                                                 871 CTTCCAGGTGAGCGGGGACTCCTGGCG------GGAGCAGAAGGAGAGGCGGG
                                                                                                                           CCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTGCTGGATCCCCTTCTTCCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351,473B
FILING DATE: 21-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 93 04670
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR94/00447
                                                                                                                                                                                                                                                                                                                        1098 AGAACTACAACAATGCCTTCAAGAGCCTCTTT 1129
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IBM PC compatible
YSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
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APPLICANT: KAPOOR, AR
TITLE OF INVENTION: B
NUMBER OF SEQUENCES:
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STRANDEDNESS: sing
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US-08-351-473B-7
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Length 1227;
Score 89.8; DB 1; Length 1 Pred. No. 2.4e-10; 0; Mismatches 442; Indels
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708 CGGGGTCACCGAAGAACCCTTCTATGCCCTCTTCTCCTCTCTGGGCTCCTTCTACATCCC 767
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APPLICANT: Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
TITLE OF INVENTION: USE OF ALPHA-IC SPECIFIC COMPOUNDS TO TREAT BENIGN
TITLE OF INVENTION: PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                              768 TCTGGCGGTCATTCTAGTCATGTACTGCCGTGTCTATATAGTGGCCAAGAGAACCACCAA
                                                                                                                                                                                                                     754 CCGCCGCGGAGAGCTGTGCTGCCGTTGCCGGCCACCATGCAGGTGAGGTCCAAGGTAAA
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13-APR-1994
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,93:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08228932
Patent No. 5578611
GENERAL INFORMATION:
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STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: (212) 422523 COOP UI INFORMATION FOR SEQ ID NO: 3:
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NAME: White, John P.
REGISTRATION NUMBER: 28,6
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LENGTH: 1738 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York COUNTRY: U.S.A. ZIP: 10112
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US-08-228-932-3
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                                                                                                                                                                    APPLICANT: Jonathan A. Bard et al.

TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
TITLE OF INVENTION: Receptors and Uses Thereof
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Pred. No. 4.2e-10;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/952,798
FILING DATE:
ATTONNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 64-0525
TELEX: (212) 42253 COOP UI INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                   Sequence 3, Application US/08334698
Patent No. 5556753
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
CITY: New York
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nucleic acid
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Best Local Similarity 48.9
Matches 366; Conservative
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                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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CLASSIFICATION: 435
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                                                                                                                                      GENERAL INFORMATION:
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                                 US-08-334-698-3
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Query Match
Best Local Similarity 48.9°
Matches 366; Conservative
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                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
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US-08-468-939-3
                                                                                                                      CITY: New York STATE: New York COUNTRY: U.S.A.
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HYPOTHETICAL: 1
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FEATURE:
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                                                                                                                                                                                     Length 1738;
                                                                                                                                                                                  Ouery Match 7.7%; Score 88.8; DB 1; Length 1 Best Local Similarity 48.9%; Pred. No. 4.2e-10; Matches 366; Conservative 0; Mismatches 362; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1101 ACTACAACAATGCCTTCAAGAGCCTCTT 1128
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US-08-468-939-3
; Sequence 3, Application US/08468939
; Patent No. 5714381
; GENERAL INFORMATION:
                                    DNA (genomic)
     single
                                                                                                                 LOCATION: 124..1683
; CTHER INFORMATION:
US-08-228-932-3
                   unknown
                                  MOLECULE TYPE: D
HYPOTHETICAL: N
STRANDEDNESS:
                                                                    Z
                                                                  ANTI-SENSE:
                                                                                                     NAME/KEY:
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48.9%; Pred. No. 4.2e-10;
Live 0; Mismatches 362; Indels 20
Jonathan A. Bard et al.
FENTION: DNA Encoding Human Alpha 1 Adrenergic
VENTION: Receptors and Uses Thereof
                                                         TITLE OF INVENTION: DNA Encoding Human TITLE OF INVENTION: Receptors and Use NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: 6 ADDRESSEE: COOPER & DUNHAM LLP STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 41337-1B TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400 TELEFAX: (212) 391-0526 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1738 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/468,939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
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814 GGAAGCACCTGATGAGGCTGAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCCTT 873

Search completed: September 7, 2004, 17:15:10 Job time : 114 secs

us-09-976-782-15.rng

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Abn86917 Human NOV
Aba01984 Human NOV
Aad29691 Human NOV
Aad2963 Human G-P
AbK71923 Human G-P
AbK71923 Human G-D
Adc86156 Human GPC
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Mouse 5-H
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                                                                                                                                                                                       US-09-976-782-15
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1 cgccatggaggccgctagcc.....aagcagagatgaacacaggg 1152
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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                                                                                                                 September
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	Abq472208 Kat KEC17 Abq43623 Oligonucl Apq43622 Oligonucl Ap42175 Nucleotid Aaq70265 Human ser Aas98116 Human DNA Aac71992 Single nu Aac71992 Single nu Aac71998 Single nu Abc71989 Polynucle Abc81689 Polynucle Abc81689993 Human gly	ENTS				ID NO:15.	cytostatic; antiarteriosclerotic; cardiovascular; lymphoma; immunosuppressive; neuroprotective; gene therapy; cancer; y; atherosclerosis; cell signal processing; diabetes; AIDS; hway modulation; neoplastic; neurological disorder; asthma; n; prostate cancer; uterus cancer; immune response; se; multiple sclerosis; Graft versus host disease; gene; ss.		s receptor-like protein"					
į	AAQV3628 ABQ43623 ABQ43623 AAGV10265 AAQV10265 AACV1995 AACV1999 AACV1999 AACV1999 AACV1999 AACV1999 AACV1999 AACV1999 AACV1999 AACV1999 AACV1999 AACV1999 AACV1999 AACV1999 AACV1999 AACV1999	ALIGNMENTS	BP.			sequence SEQ	arterioscle ve, neuropr is; cell si neoplastic er, uterus erosis; Gra		н					
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	1116 631111 71118 8 4 4 5 2 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		; cDNA;		st entry)	Ig cDNA	static inosup; cheros modul costati multip		Location/Qualifie 51144 /*tag= a /product= "NOV5" /note= "Serotonin			2001WO-US03	44444444444444444444444444444444444444	
	100800080000000000000000000000000000000		standard;		first	encoding	ytost immun i atl way i i pro e; m		7.5			0011	00000000000000000000000000000000000000	, ii
1	80000000000000000000000000000000000000		and		J)	ence	; c; thy athy oma east	w		-A2				E
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	O		RES ABB XX	X X	TO X	DE		80 \$		Y M S	(1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	주 전 당	X X X X X X X X X X X X X X X X X X X	X X

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Ellerman K; Spytek KA; New NOVX polypeptides and polynucleotides, useful for treating or preventing a NOVX-associated disorder or a pathological state in a subject, particularly a human, e.g. cardiomyopathy, atherosclerosis, cancer or diabetes. cok JP, lepley DM, Burgess CE, Mishra V; Padigaru M, Shimkets RA, Zerhusen BD, Sp .h V. Macdougall J, Stone D, Gunther E, 9; Page 46; 227pp; English. Alsobrook JP, Li L, Padig Gerlach V, WPI; 2002-444172/47. P-PSDB; ABB78809. Grosse WM, Kekuda R, I Edinger S, Claim

The present invention describes novel human proteins designated NOVX (where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a tyrosine-protein kinase 6-like protein; NOV24 are keratin 4-like protein; NOV35 is a collagen-like protein; NOV44 is a cystatin B-like protein; NOV95 is a serotohin receptor-like protein; NOV65 and NOV65v are cold inducible glycoprotein 30-like protein; NOV9 is a matrilin-2-like protein; NOV9 is a leukcyte surface antigen (CD53)-like protein; and cold inducible glycoprotein 30-like protein; NOV9 is a tyrosine kinase-like protein. NOVX sequences have cytostatic, antiarteriosclerotic, cardiovascular, antidiabetic, immunosuppressive and continuous can be used in therapeutics, particularly for treating, sequences can be used in therapeutics, particularly a thuman. These disorders include cardiomyopathy, atherosclerosis, a disorder related to cell signal cardiomyopathy, atherosclerosis, a disorder related to cell signal processing and metabolic pathway modulation or diabetes. The NOVX sequences are also useful for determining the presence of or predisposition to a disease associated with altered levels of NOVX collypeptide or nucleic acid, particularly cancer. The NOVX sequences are expecially useful in therapeutic or prophylactic applications for a neoplastic or neuropagated isorders, and in the treament of experience of the processing and metabolic pathway and in the treament of experience of the processing and the presence of the particularly cancer. The NOVX sequences are necessarially are acid, particularly cancer. The NOVX sequences are necessarially and in their application or interest and in the presence of the processing and interest leaded to the presence of the necessarial particularly and in the treatment of a material particularly and in the presence of the particularly and in the presence of the particularly and the presence of the nove of the particularly and the presence of the particular and the particular and the particular and the particular and the particular adenocarcinoma, lymphoma, prostate cancer, uterus cancer, immune response, AIDS, asthma, Crohn's disease, multiple sclerosis or Graft versus host disease. The present sequence encodes the human NOV5 protein from the present invention. NOV5 is located to chromosome 2

Sequence 1152 BP; 176 A; 388 C; 359 G; 229 T; 0 U; 0 Other;

ö 120 120 180 180 240 240 300 300 360 420 420 09 9 1 CGCCATGGAGGCCGCTAGCCTTTCAGTGGCCACCGCCGGCGTTGCCCTTGCCCTGGGACC ceacaccaccaccacccccaacccccaaccccaacacacaaracrcccarcaccccaac GCTGCTAGTGCTGCTGCTGCTGCCACTTTCCTGTGGAACCTGCTGCTGCTGTCCGGTCACTA CCCGCGGGTCCCTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTCTC GGACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCTGGCGAGTGAGCTGTCGACCGG GGACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGG GCGACGTCGGCTGGCCCGGAGCCTGTGCCACGTGTGGATCTCCTTCGACGCCGGAGC GCGACGTCGGCTGCTGGGCCGGAGCCTGTGCCACGTGTGGATCTCCTTCGACGCCGGAGC CGCCATGGAGGCCGCTAGCCTTTCAGTGGCCACGCCGCGCGTTGCCCTTGCCCTGGGACC CGAGACCAGCAGCGGGACCCCCAAGCCCGAGAGGGATACTCGGTTCGACCCCGAG GCTGCTAGTGCTGCTGATCGCTGCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCACCAT CCCGCGGGGTCCGTGCCTTCCACCGCGTGCCCATAACTTGGTGGCCTCGACGGCCGTCTC Gaps ; Length 1152; Indels 100.0%; Score 1152; DB 6; 100.0%; Pred. No. 7.4e-240; iive 0; Mismatches 0; 0; Query Match Best Local Similarity 100. Matches 1152; Conservative Н 61 19 121 181 241 241 301 301 121 361 181 g g Db qq à g à ò δ δ d à δ

1080 1020 840 840 900 900 960 099 099 720 720 780 780 480 009 009 immune disorder; haematopoietic disorder; developmental disease; cancer; retinal disease; feeding disorder; vaccine; infection; gene therapy; neurological disorder; psychotic disorder; G-protein coupled receptor; cytostatic; antidiabetic; virucide; neuroprotective; noctropic; analgesic; antidepressant; antimigraine; anticonvulsant; neuroleptic; antipsoriatic; antiallergic; antiniflammatory; anorectic; antiarthritic; antipsoriatic; antiatherosclerotic; antidacterial; fungicide; osteopathic; protozoacide; antiulcer; hypertensive; hypotensive; antiinfertility; vulnerary; nephrotropic; antilipemic; ceccrrcrccacceeeeeeccrrccaccreccecrreecareccerreice GTTCACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGGGA GCAGAAGGAGGCGAGCAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTG GCAGAAGGAGGGGGGGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTG TTACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAG TTACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAG CTGTCTGTGCTGCCCCGCCGGCCTCGGGAACGTGGCGGCCATCGCCCTGGGCCGCGACGG GATOGCGCTCGCCCGGGTGCCGTCGCCCTCATCGCCCTCGCGCCGCTGCTTTTGGCCG GGGCGAGGTGTGCGACGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCCTATGC COCCITICACCCGCGCGCCTTCCACCTGCCGCTTGGCGTGCTCCCGTTTGTCTACCG GAAGATCTACGAGGCGGCCAAGTTTCGTTTCGGCCGCCGCCGGAGAGCTGTGCTGCCGTT GCCGGCCACCATGCAGGTGAGGTCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGTGGT 841 GTTCACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGGGA crercirerectececececereseaaceresececearesecereseceeeeeee GGCCATCACACGGCACCTGCACACGCTGCGCACCCGCGCCGCGCCTCGTTGCTCAT Human; NOV5a; metabolic disorder; neurodegenerative disorder; BP ABA01984 standard; cDNA; 1150 Human NOV5a coding sequence. ATGAACACAGGG 1152 1141 ATGAACACAGGG 1152 (first entry) 12-FEB-2002 781 (1021 1081 1141 ABA01984; 196 661 661 901 196 1021 1081 421 481 541 601 601 721 781 841 901 421 481 ABA01984 RESULT g g q ò d d 유 à ð g à g à 엄 à qq à Db 8 셤 ઠે ð à à

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                                                                                                                                                                                                     TTACACAGGTTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAG 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; G-protein coupled receptor; GCREC-15; cell proliferative disorder; neurological; cardiovascular; gastrointestinal; autoimmune; inflammatory; metabolic; hepatitis; psoriasis; cancer; ppilepsy; Alzheimer's disease; pick's disease; Huntington's disease; Parkinson's disease; hypertension; atherosclerosis; myocardial infarction; gastritis; cirrhosis; cytostatic; osteoporosis; Crohn's disease; acquired immunodeficiency syndrome; AIDS; anaemia; asthma; rheumatoid arthritis; diabetes; obesity; drug screening; transgenic animal; allergy; gene therapy; hepatotropic; aniconvulsant; nootropic; neuroprotective; cardiant; immunosuppressive; anorectic;
                GCAGAAGGAGGGGGGGGGGCGAGGAGGAGGGGGAATTCTGATTGGCGTTTGTGCTGTG 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patterson C, Lal P, Burford N, Yue H, Gandhi AR;
Ramkumar J, Baughn MR, Kallick DA, Walia NK, Hafalia AJA;
                                                                          CTGGATCCCCTTCTTCCTGACGGAACTCATCAGCCCACTCTGTGCCTGCAGCCTGCCCCC
GCAGAAGGAGAGGCGAGCAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTG
                                                        CTGGATCCCCTTCTTCCTGACGGAACTCATCAGCCACTCTGTGCCTGCAGCTGCCCCC
                                                                                                                                           /*tag= c
/product= "Human mature GCREC-15"
                                                                                                                                                                                                                                                                                                                                                                                                                            Human G-protein coupled receptor (GCREC-15) cDNA.
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/product= "Human GCREC-15"
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1. .1113
                                                                                                                                                                                                                                                                                                                                       AAD29681 standard; cDNA; 1458 BP
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2000US-0232243P.
2000US-0232691P.
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2000US-0227054P.
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/*tag= b
196. .1110
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                                                                                                                                                                                                                                  ATGAACACAGGG
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13-SEP-2000;
15-SEP-2000;
22-SEP-2000;
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21-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                               17-MAY-2002
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901
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The invention relates to novel human G-protein coupled receptors (GCREC) and their encoding polynucleotides. GCREC is useful as an immunogen for preparing monoclonal and polyclonal antibodies. GCREC is useful for diagnosing, treating and polyclonal antibodies. GCREC is useful for diagnosing, treating and polyclonal artibodies. GCREC is useful for hepatitis, psoriasis, cancer), a neurological disorder (e.g., palepsy, Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's disease), a cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infarction), gastrointestinal disorder (e.g., gastritis, cirrhosis, Crohn's disease), an autoimmune/ inflammatory disorder (e.g., acquired immunodeficiency syndrome (ALDS), allergy, anaemia, asthma, rheumatoid arthritis), a metabolic disorder (e.g., diabetes, obesity, osteoporosis), and viral infactions. GCREC is useful in a number of drug screening techniques, and to analyse the proteome of a tissue or cell type. GCREC is useful for creating knockin humanised animals or transport animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation,
                                                                                                                                                     New human G-protein coupled receptor polypeptide for diagnosis, prevention and treatment of cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune/inflammatory, and metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inversion, etc., among normal, carrier or affected individuals, and as hybridization probes for mapping naturally occurring genomic sequences. GCREC is useful in Southern or northern analysis, dot blot or other membrane-based technologies, in PCR technologies, in dipstick, pin, multiformat enzyme linked immunosorbant (ELISA)-like assays, and in microarrays utilising fluids or tissues from patients to detect altered GCREC expression. The present sequence is human GCREC-15 cDNA
  Graul RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1458 BP; 262 A; 447 C; 433 G; 316 T; 0 U; 0 Other;
     Kearney L,
Policky JL,
                                                                                                                                                                                                                                                                                       Claim 5; Page 148; 150pp; English.
  υ,
Έ
  Y, Tribouley
Lee EA, Ding
                                                                              2002-188744/24
                                                                                              P-PSDB; AAE18654
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                           BA,
                                                                                                                                                                                                                                      disorders.
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     Yao MG,
Warren 1
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Gaps 27; 0; Indels Score 1064; DB 6; Pred. No. 8.8e-221; 0; Mismatches 0; 92.4%; Matches 1121; Conservative Similarity Local

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The invention relates to isolated human G-protein coupled receptor (GCREC) polypeptides and their biologically active fragments. GCREC and protein is useful in treating a disease or condition associated with an increase or decrease in expression of functional GCREC. The GCREC's are useful in the diagnosis, treatment and prevention of cell proliferative disorders (cancer, leukaemia, melanoma); neurological disorders (stroke, epilepsy, Parkinson's disease, dementia, Alzheimer's disease); autoimmune inflammatory disorder (thyroiditis, haemolytic anaemia, AIDS, multiple sclerosis); cardiovascular disorder (atherosclerosis, angina pectoris), metabolic disorders (diabetes); viral inflections (herpes virus) and in the assessment of the effects of exogenous compounds on the expression of the nucleic acid and amino acid sequences. The present sequence is human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated human G-protein coupled receptor polypeptides and the use of these sequences in the diagnosis, treatment and prevention of diseases and in the assessment of exogenous compounds on the expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gandhi AR, Kallick DA,
Lu DAM, Tribouley CM,
Ramkumar J, Au-Young J;
ky ML, Thornton M, He A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ACCAGCAG-----CGGGACCCCAAGCCCGAGAGGATACTCGGTTCGACCCCGAGCGGC
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Patterson C, Lu DAM,
to MG, Yang J, Ramkum.
sh RT, Borowsky ML,
     '*tag= a
'product= "Human GCREC-8 protein"
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Pred. No. 6.1e-220;
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                                                                                                                                                   "Mature GCREC-8
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raul R, Yao MG, Y
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22-JUN-2000; 2000US-021354P.
29-JUN-2000; 2000US-0215209P.
07-JUL-2000; 2000US-0218358P.
14-JUL-2000; 2000US-0218936P.
19-JUL-2000; 2000US-0218936P.
21-JUL-2000; 2000US-0219354P.
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The invention relates to an isolated NOVX polypeptide selected from NOV1a, NOV1a, NOV1a, NOV2b, NOV2c, NOV3a, NOV3b, NOV4b, NOV4b, NOV5c, NOV3b, NOV5b, NOV6b, NOV7, NOV7, NOV7, Nov6ctor comprising the nucleic acid, a cell comprising the vector; an anti-activity of NOV7, the nucleic acid, antibody and identifying agents that modulate the expression or activity of NOV7, the nucleic acid, antibody and modulators are useful in the diagnosis, treatment or prevention of developmental disorders, endocrine disorders, vascular disorders, infectious disease, reproductive disorder; tissue disorder; thrombocytopaenia; migraine; angiogenesis; asthma; X-linked severe combined immunodeficiency; inflammation; autoimmune disorder; immune disorder; blood disorder; haematopoietic disorder; gastrointestinal disease; respiratory disorder; hepatitis; fertility; hypertension; arteriosclerosis; ischaemia; rheumatoid arthritis; Grave's disease; wound healing. New cytoplasmic, nuclear, membrane bound and secreted NOVX polypeptides, useful for treating cancers and tumors, lung disorders, hematopoietic disorders, autoimmune diseases and immune disorders. vascular disorder, infectious disease, anorexia, cancer, stroke, neurodegenerative disorder, Alzheimer's disease, acute brain injury, central nervous system disorder, depression; lung disorder; endocrine disorder; Syptek KA, Taupier RJ, Vernet CAM, Colman SD; hernev VT, Malyankar UM, Shenoy S, Tchernev VT; Patturajan M, Burgess CE, Smithson G, Millet I; stone D, Gunther E, Ellerman K; Vernet CAM, C developmental disorder; Claim 9; Page 59-60; 210pp; English. 15-SEP-2000; 2000US-0232675P.
15-SEP-2000; 2000US-0232676P.
18-SEP-2000; 2000US-023362P.
18-SEP-2000; 2000US-0233802P.
19-SEP-2000; 2000US-0233521P.
19-SEP-2000; 2000US-0233521P.
19-SEP-2000; 2000US-0233501P.
19-SEP-2000; 2000US-0233801P.
20-SEP-2000; 2000US-0233960P.
20-CT-2000; 2000US-0238396P.
13-OCT-2000; 2000US-0240284P. 11-JAN-2001; 2001US-0260973P. 26-JAN-2001; 2001US-0264274P. 17-SEP-2001; 2001WO-US029115 09-MAR-2001; 2001US-0274862P Tchernev VT, gene; NOVX; Syptek KA, Sorman .., Padigaru M, Pattu., -- .TA. Stone D, (CURA-) CURAGEN CORP. WPI; 2002-383182/41. P-PSDB; ABG60235 40200224733-A2 Homo sapiens. 28-MAR-2002 Mishra VS,

anorexia, cancer, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, multiple sclerosis and amyotropic lateral sclerosis), acute brain injury (e.g. stroke, head injury and cerebral palsy), central nervous system disorders (e.g. depression, epilepsy and schizophrenia), lung disorders, reproductive disorders, disorders affecting carbohydrate metabolism (e.g. Wiskott-aldrich syndrome, thrombocytopaenia, night blindness and pick's disease), disorders linked to abnormal angiogenesis, asthma, azospermia, learning disabilities, facial dysmorphism, autoimmune encephalomyelitis, X-linked severe combined immunodeficiency, seizures, migraines, inflammation, autoimmune disorders, disorders affecting sleep,

Human cDNA encoding hydroxytryptamine receptor-like protein NOV8.

30-JUL-2002 (first entry)

BP.

standard; cDNA; 1155

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                                                                                                                                                                                                                                                                                                                                                                  1058 TCCAATTCTTTCTTCAACCCCCTGATTTACACAGGCTTTTAACAAGAACTACAACAATGCC
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Gaps

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atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy; chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease; depression; epilepsy; macular degeneration; lymphoma; malanoma; multiple sclerosis; osteoarthritis; osteoporosis; parkinson's disease; psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis; tuberculosis; cognition disorder; memory disorder; anorexia; hormonal release disorder; cardiovascular activity disorder; pain perception disorder; obssity; diabetes; obesity; diabetes; hyperlipidaemia; stroke; gene therapy.

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Novel G protein-coupled receptor polypeptides including galanin receptor polypeptides useful for identifying modulators that are useful for treating Alzheimer's disease, psoriasis, melanoma, multiple sclerosis,

Disclosure; Page 119-120; 144pp; English.

stroke.

Pritchard

Fabre-Suver C,

Burmer G,

Miller M,

Brown JP,

WPI; 2002-066595/09

(LIFE-) LIFESPAN BIOSCIENCES INC.

18-MAY-2000; 2000US-0205945P.

11-MAY-2001; 2001WO-US015332 11-MAY-2000; 2000US-0203217P

WO200185791-A1. Homo sapiens

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The invention relates to an isolated polypeptide encoded by a nucleic acid molecule that is at least 80% identical to the G protein-coupled (GPCR) polynucleotides included in the specification. Also included are probes based on the GPCR sequences (including antisense probes), a host cell comprising an expression vector comprising the GPCR sequences (call comprising an expression vector comprising the GPCR sequence).

CC call comprising an expression vector comprising the GPCR sequence. C antibodies raised against the polypeptides, and methods of identifying modulators or metagonists of the polypeptides are useful for repressors, agonists or antagonists of the novel GPCR polypeptides or including the GAM4 polypeptide. The antibodies and nucleic acid probes as corrected and nucleic acids and are used to detect the presence of the polypeptides and nucleic acids and are used to detect the presence of the polypeptides and nucleic acids and are used to diagnose a variety of diseases or disorders in which GPCRs are involved e.g., Altheimer's disease, cardinoma, breast carcinoma, cardiomyopathy, chondrosarcoma, chronic obstructive pulmonary disease, Crohn's disease, psoriasis, rheumatoid architis, schizophrenia, ulcerative colitis, tuberculosis and many other costeoarthritis, osteoporosis, Parkinson's disease, psoriasis, rheumatoid arthritis, schizophrenia, ulcerative colitis, tuberculosis and many other cuseful for diagnosing cognition and memory disorders, pain perception disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds that decrease or increase the expression of galanin receptor (GAL4) can concleic acid is useful for treating the above mentioned disorders by gene to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR nucleic acid is useful for treating the above mentioned disorders by agenetic physelenger.
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94.6%; Pred. No. 9.6e-152;
iive 0; Mismatches 20;
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Human, G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor; Alzheimer's disease; amyotrophic lateral sclerosis; asthma;

Human DNA for potential G protein-coupled receptor #11

(first entry)

12-MAR-2002

AAS98053;

ВР

AAS98053 standard; DNA; 977

AAS98053

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Oligonucleotides corresponding to conserved regions of known serotonin receptors were used in PCR of mouse brain RNA in presence of reverse transcriptase and the products were sequenced. One product with homology to known receptors was labelled and used to probe a CDNA library in Lambda UniZAP. The 2036 bp sequence AAA70264 was identified and deduced to encode a protein having 7 hydrophobic domains which represents a novel serotonin receptor which was designated 5HT5b. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCAGCAGCGGACCCGGGACCCCGAGGCCCGAGGGATACTCGGTTCGACCCCGAGCGGC 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New serotoninergic receptor 5HT5b and related nucleic acid and recombinant cells - useful for treatment and diagnosis of e.g. neurological or cardiovascular disease, also for identifying sagonists and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.6%; Score 732.8; DB 2; Length 2036; 79.9%; Pred. No. 4.9e-149; ive 0; Mismatches 202; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2036 BP; 425 A; 582 C; 542 G; 487 T; 0 U; 0 Other;
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                               location/Qualifiers
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                                                                                                      "SHT5b"
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The present invention relates to transgenic animals, compositions and methods relating to the characterisation of gene function. The invention also relates to transgenic mice comprising mutations in 5-hydroxy-tryptophan (5-HT)5B receptor gene. The transgenic mice are useful for identifying an agent that modulates the phenotype such as increased identifying no rential therapeutic agents for the treatment of pain or depression or increased pain sensitivity. They are also useful for identifying potential therapeutic agents for the treatment of pain or depression and for evaluating a potential therapeutic agent capable of affecting a condition associated with a mutation in a 5-HT5B receptor gene. Transgenic animals of the invention are also useful for testing the
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Serotonin, receptor; transmembrane, domain, kinase; phosphorylation, sensory; motor; behaviour; central nervous system; CNS; superfamily; d-protein; ligand-gated; ion channel; subfamily, human, rat; amplify; primer; PCR; amplification, brain, hypothalamus; indolamine, drug; hypothalamus; therapeutic; neurological; pathology; dementia; insomnia; Parkinson's disease, eating disorder; anxiety; migraine; headache; ss. BP. Rat MR22 serotonin receptor gene. AA072270 standard; cDNA; 2226 (first entry) 25-MAR-2003 24-MAY-1995 AAQ72270;

360 122 414

Gaps

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Conservative

Local Similarity

Query Match

911; m

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Score 729.8; DB 2; Pred. No. 2.2e-148; Mismatches

63.4%;

Length 2226;

301 CAATGGAAGTCTCTAACCTCTCAGGCGCCCACCCTGGCATTGCCTTTCCTCCGGGACCCG AGACCAGCAGCGGACCCGGGCACCCCGAGGCATACTCGGTTCGACCCCGAGCG 361 AGAGCTGCAGTGAC----AGCCCAAGTTCCGGCAGAAGCATGGGATCCACCCCAGGGG

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123 GCGCCGTCCTGCCGGGCCGAGGCCGCCCTTCTCTGTCTTCACGGTCCTGGTGGTGACGC 182

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The nucleotide sequence of the novel rat serotonin receptor MR22. The gene encodes a protein of 370 amino acids. The protein contains 7 can semicate domains (TMDS), a putative N-linked glycosylation site and 4 putative sites for kinase C phosphorylation. Serotonin receptors a wide range of sensory, motor and behavioural functions in the central nervous system (CMS). Serotonin receptors belong to at least two protein superfamilies: G-protein-associated receptors containing 7 TMDs (S-HT13). The serotonin receptors presented in the patent represent prototypes that fall into three new serotonin subfamily classifications: 5-HT16-like (rat MR77 - AAQ72271 and human MR77 - AAQ72271), 5-HT5 (subdivided into 5-HT5alpha, rat REC17 - AAQ72269 and 5-HT5 (brote by see cloned by amplification based on conserved amino acid sequences and used in two rounds of nested PCR amplification on a crat brain hypothalamic cDNA template. In the second round of amplification degenerate primers corresponding to conserved residues found in the TMDs. Degenerate primers were cloned into pBluescript cond and their corresponding proteins may be used in methods for determining ligand binding activity, detecting and altering expression of serotonin correctors, receptors, detecting and altering expression of serotonin receptors; detecting and their corresponding proteins may be used in methods for determining and electronic receptors.
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                                                                                                       "rat MR22 serotonin receptor"
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The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox mean values.
                                                                                                                              diagnostic marker;
                                                                                               Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:2961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor; Alzheimer's disease; amyotrophic lateral sclerosis; asthma; atherosclerosis; basal carcinoma; breast carcinoma; cardiomyopathy; chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease; depression; epilepsy; macular degeneration; lymphoma; melanoma; multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disease; psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis; tuberculosis; cognition disorder; memory disorder; anorexia; hormonal release disorder; cardiovascular activity disorder; hormonal release disorder; obesity; diabetes; obesity; diabetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders in which GPCRs are involved e.g., Altheimer's disease, amyGrophic lateral sclerosis, asthma, atherosclerosis, basal cell carcinoma, breast carcinoma, cardiomyOpathy, chondrosarcoma, chronic obstructive pulmonary disease, Crohn's disease, depression, epilepsy.
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arthritis, osteoporosis, Parkinson's disease, psoriasis, rheumatoid arthritis, schizophrenia, ulcerative colitis, tuberculosis and many other diseases listed in the specification. The probes and antibodies are also useful for diagnosing cognition and memory disorders, anorexia, hormonal release disorders, cardiovascular activity disorders, pain perception disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds be used to increase the expression of galanin receptor (GAL4) can be used to treat obesity, hyperlipidaemia and stroke. The GPCR nucleic acid is useful for treating the above mentioned disorders by gene therapy techniques. The present sequence is a novel GPCR polymucleotide
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Pred. No. 1.4e-146;
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                                                                                                                                                                                                    Sequence 1090 BP; 157 A; 364 C; 372 G; 197 T; 0 U; 0 Other;
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                                                                                                        Human; 5-hydroxytryptamine receptor 5A; HTR5A; serotonin; gene; ds; neuroprotective; neurological disease; depression; epilepsy; gene therapy; single nucleotide polymorphism; haplotype pair; chromosome 7q36.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel genetic variants of 5-Hydroxytryptamine (Serotonin) Receptor isogenes, useful for improving efficiency and reliability in drug development for treating neurological diseases.
                                                                                                                                                                                                                                                        "Single nucleotide polymorphism"
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         the HTRSA haplotypes given in the specification or whether both copies are defined by a haplotype pair. This method is useful in genotyping, whereby all possible haplotype pairs can be assigned to specific genotypes. An association between a trait and a haplotype or haplotype pair of the HTRSA gene can be identified by comparing the frequency of the haplotype pair in a population exhibiting the trait with the frequency of the haplotype pair in a population exhibiting the trait with indicates the trait is associated with the haplotype or haplotype pair in a reference population, where a higher haplotype frequency in the trait population indicates the trait is associated with the haplotype or haplotype pair. HTRSA and its corresponding DNA are used for studying the expression and function of HTRSA, and in screening for candidate drugs to treat diseases related to HTRSA activity, such as neurological disorders, including depression and epilopsy. This sequence represents the DNA encoding the human HTRSA polypeptide
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 gene is defined by one of
                                                                                                                                                                                                                                                                                                                        113 ACCCCGAGCGCCCCCTCCTGCCGGCCCGAGGCCGCCCTTCTCTGTCTTCACGGTCCTG
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                                                                                                                                                                                                                                                              DB 6; Length 1074;
                                                                                                                                                                                                                                    Sequence 1074 BP; 182 A; 366 C; 284 G; 242 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                              Score 497.6; DB 6;
Pred. No. 3.6e-98;
0; Mismatches 279;
 the copies of the
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Best Local Similarity 70.6%;
Matches 729; Conservative
 whether one of
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G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; grotein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn; disease; diabetes; graft versus host disease; parimon; schizophrenia; dementia; memory loss; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; hypertension; hypertension; schizophrenia; dementia; rausea; ulcer; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
TGGCGGGAGCAGAAGGAGAGAGCGAGCCATGATGGTGGGGAATTCTGATTGGCGTGTTT
                                                           823 TGGCGGGAGCAGCAGCAGCGGCCGCCCTCATGGTGGGCATCCTCATTGGCGTTC
                                                                                                                                                                                                                              1003 CCCCTGATCTATACGGCTTTCAACAAGAACTACAACAGCGCCTTCAAGAACTTCTTTTCT
                                                                                                                                                              GTGCTGTGCTGCATCCCCTTCTTCCTGACGGAACTCATCAGCCCCACTCTGTGCCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                             943 ATCCCCGCCATCTGGAAAAGCATCTTCCTGTGGCTTGGCTACTCCAACTCCTTCTTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCCTGATTTACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACT
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P-PSDB; ABP81980.
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avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for CC tracting immune-related diseases, jenuth-related diseases, for all regeneration-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, growth-related cell proliferative corresponding immune-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, catherosclerosis, bacterial, fungal, protozcan or viral infections, catherosclerosis, bacterial, fungal, protozcan or viral infections, catherosclerosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, crohn's disease, diabetes, graft versus host disease, parkinson's disease, multiple sclerosis, pain, psoriasis, cancer, contractive depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or used in immunoassays and immunodiagnosis. ABZ42523 to ABZ425869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the present invention

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Sequence 1074 BP; 182 A; 366 C; 284 G; 242 T; 0 U; 0 Other;

Ouery Match
Best Local Similarity 70.6%; Pred. No. 3.6e-98;
Matches 729; Conservative 0; Mismatches 279; Indels 24; Gaps 4;

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Search completed: September 7, 2004, 15:10:54 Job time : 507 secs This Page Blank (uspto)

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Database

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Homo sapiens HTRSA gene, VIRTUAL TRANSCRIPT, partial sequence, AY402561.
AY402561.1 GI:39758547
                       AL344524 TELEROGON BLG0344448 BC031272 Home sapi BC715343 602677361 BE6715343 602677361 BE6715343 602677361 BE628489 BE628233 AL922333 BE63529 BE653529 AR402233 BE63529 BE653529 AR402237 BC827135 GO2756117 BC827135 GO27561107 BC827135 GO27561107 BC827135 GO27561107 BC827135 GO27561107 BC827135 GO27561107 BC827135 GO27561107 AR418851 Home sapi AR409287 Home sapi BRO26157 AGENCOURT AY409287 Home sapi BC018330 Mus muscu AK004891 Mus muscu AK04891 Mus muscu AK048977 Mus muscu
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1 (bases 1 to 1074)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Andd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Toda, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
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AY399426 H
AY418220 M
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                                   B1603546
BC031272
B1538349
BG715343
B1411238
BB621710
CD600820
CE490868
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CB565883
BB653529
AY402238
                                                                                                                                                                      CNS018EH
AY402237
CB784054
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BI195997
BQ879192
BQ719305
AY418851
AQ897350
AY418853
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BI820920
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BM926157
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BC018330
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Homo sapiens
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DEFINITION
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
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KEYWORDS
SOURCE
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AY402561 Homo sapi
AY402562 Pan trogl
BZ601879 WHAAAS5TF
AY402563 Mus muscu
                                                           5; Search time 2862 Seconds
(without alignments)
12019.997 Million cell updates/sec
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                                                                                                                                                                                 55026578
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                               27513289 segs, 14931090276 residues
                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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                                                            7, 2004, 15:11:05
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Maximum Match 100%
Listing first 45 summaries
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AY402562
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                                          nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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495 477.6 426.2

Score 496

Result No.

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GIGCIGIGCIGGAICCCCIICTICCIGACGGAACICAICAGCCCACICIGIGCCIGCAGC 1012
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Pan troglodytes HTR5A gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 ATTCTCACCTTGCTGGGCTTTCTGGTGGCGGCGACGTTCGCCTGGAACCTGGTGCTG 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1074)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark.A.G., Glancowski,S., Nielson,R., Thomas,P., Kejariwal,A., Clark.A.G., Glancowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Adams,M.D. and Cargill,M. Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                                                                                                                                                                                                                               CCCCTGATTTACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACT
                                                                          CTGCCCCCCATCTGGAAAAGCATATTTCTGTGGCTTGGCCTACTTCCATTCTTTCAAC
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Pred. No. 3.3e-80;
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/locus_tag="HCM1265"
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Location/Qualifiers
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Pred. No. 2.2e-80;
0; Mismatches 280;
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/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
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ilarity 70.5%;
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Best Local Similarity
Matches 728; Conserv
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Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates, Catarrhini; Hominidae; Homo. 1 (bases 1 to 640) Volik, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, Q., Kowbel, D., Huang, G., Lapuk, A., Kuo, W.-L., Magrane, G., de Jong, P., Gray, J.W. and Collins, C.
End-sequence profiling: Sequence-based analysis of aberrant genomes 22709111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (WCF7_1)"
/note="Vector: pECBAC1; Site_1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."
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Pred. No. 4.3e-77;
0; Mismatches 19; Indels 26;
                                                                                                                                                                                                                                                                                            Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
                                                                                                                                                                                                                                           94143-0808,
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Colin Collins' lab
COLIN Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94
Tel: 415 502 7066
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
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| organism="Homo sapiens" |
| mol type="genomic DNA" |
| db zref="taxon:9606" |
| clone="MNF7 1-1113" |
| sex="female"
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Class: BAC ends.
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Best Local Similarity 92.2%;
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can febund through the I.M.A.G.E. Consortium/LIML at:
http://image.llnl.gov
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wano, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       AY402563 1074 bp DNA linear GSS 15-DEC
Mus musculus HTR5A gene, VIRTUAL TRANSCRIPT, partial sequence,
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                                                                                                                   784 GGCCACCATGCAGGTGAGGTCCAAGGTAAAGGAAGCACCT
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1.1074
/organism="Mus musculus"
/mol type="genomic DNA"
/db_xref="taxon:10090"
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Bukaryota, Metazoa, Chordata,
Mammalia, Butheria, Rodentia,
1 (bases 1 to 1074)
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV destroyed); Site 2: Not1; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."
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0; Mismatches 153; Indels 12;
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/clone="IMAGE:5731557"
/tissue_type="hippocampus"
/lab_host="DH10B"
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    column:
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High quality sequence stop: 616.
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BI489745 906 bp mRNA linear EST 28-AUG-2001 603032245F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173354 5',

mRNA sequence. BI489745

DEFINITION RESULT 6 BI489745

LOCUS

ACCESSION

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/lab host="MB108"
/lab host="MB108"
/clone lib="NHH MGC 115"
/note="Torgan: pooled brain, lung, testis; Vector:
/note="Torgan: pooled brain, lung, testis; Vector:
pcMV-SPORT6; Sited 1: Not1; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age 89. Library is
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I thases I to 90% I longoni, III hases I to 90% I longoni, III hases I to 90% I longoni, III hases I longoni, III has I longoni, III has I longoni, III has I longoni I lostitutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                        Context: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1431 row: j column: 11
High quality sequence stop: 826.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                           Unpublished (1999)
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1027 bp DNA linear GSS 01-SEP-2000 nigroviridis genome survey sequence T3 end of clone library A from Tetraodon nigroviridis, genomic survey
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Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                     GGGGCGAGGTGTGCGACGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCCTATG
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IMAGE:5173354, mRNA sequence.
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                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (base; Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (base; Eutheria, Primates, Catarrhini, Hominidae, Homo.

Ebert, E., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radeloć, U., Schneider, D. and Korn, B.

Human Unigeneset - RZPD3

Unpublished (2003)

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld $80, D-69120 Heidelberg, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer:
                                                                                                   RZPDLIB; I.M.A.G.E. CDNA. Clone Collection;
RZPDLIB; I.M.A.G.E. CDNA. Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cg1-
bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Resourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (cloneGarzpd.de) for further information. Seq prin
M13u, Primer sequence: CGTTGTAAAACGACGCCAGT.
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23.0%; Score 265.4; DB 13; Length 539;
Best Local Similarity 70.4%; Pred. No. 2.4e-38;
Matches 388; Conservative 0; Mismatches 151; Indels 12;
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/organism="Homo sapiens"
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EX280849.1 GI:28614119
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                                                                             Genoscope.

Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Genoscope sequence ID : COAA038BH09A1~end : T3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Tetraodon nigroviridis"
/mol type="genomic DNA"
/db_xref="taxon:99883"
/clone="038018"
/clone_lib="A"
                                                              (bases 1 to 1027)
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                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs.rement: Miklos Palkovits, M.D., Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paluescript KS+); Site 1: BamH1; Site 2: Sal1-XhoI (gtcgag); Oligo-dr primed using primer 5. "TTTTTTTTTTTTTTTTTVA-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this: a NIH_MGC Library."
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
BI603546 893 bp mRNA linear EST 07-SEP-29
603244448F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5287138 5',
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                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
/clone lib="NIH MGC 96"
/note="Organ: brain; Vector: pBluescriptR (modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11725 row: o column: 11
High quality sequence start: 2
High quality sequence stop: 720.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="hypothalamus"
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5287138"
                                                                                                 BI603546
BI603546.1 GI:15496485
                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          엄
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     517 TCCTGATACTTGTTTTACTCTTGCTGGGGCTTTCTGGTGGCGGCGACGTTCGCCTGGAACC 458
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Sasas, B., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Banastt, G.L., Heaton, W.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Reele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore
                                                          TGCTGGTTCCGGTCACCATCCCGCGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGG
                                                                                                       457 IGCTGGTGCTGCGCATCCTCCGTGTACGCACCTTCCACCGCGTGCCCCACAAACCTGG
                                                                                                                                                            TGGCCTCGACGCCCGTCTCGGACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGG
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
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Seg primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
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Fax: 402 762 4390
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Bos taurus
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235 TAGCCCTGGACCGCTACTGGTCCATCACGCGCCACATGGAATACACGCTCCGCACCGCA 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

Tobhiyuki and Piero Carninci (RIKEN)

Toshiyuki and Piero Carninci (RIKEN)

DNA Sequencing by: The I.M.A.G.B. Consortium (LINL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 943(

Web Sitie: (Dickson, Mark) med@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2683)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (03-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: IRAR Plate: 63 Row: 1 Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                            175 AGTGCGTCTCCAACGTCATGATCGCGCTCACCAGGGCACTCTCCGCTGTCATCTCTCTGG
                                                                                                                                                                                                                                 ccccccracraringecreaceacaaceracracracaccaacaacaacaacaacaacaa
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                                                                               GCCGCGCCCTCGTTGCTCATGATCGCGCTCGCCCGGGTGCCGTCGGCGCTCATCGCCCTCG
                                                                                                                                                                                    582 GGCGGCTGCTCTTTGGCCGGGGGGAGGTGTGCGACGCTCGGCTCCAGCGCTGCCAGGTGA
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                                                                                                                                                                                                                                                                                    642 GCCGGGAACCCTACCTATGCCGCCTTCTCCACCCGCGCGCCTTCCACC 689
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Location/Qualifiers
1. .2683
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/db_xref="taxon:9606"
/clone="IVAGE:5287138"
/clone="type="brain, hypothalamus"
/clone lib="NHH MGC_96"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      2683 bp mRNA
Homo sapiens, clone IMAGE:5287138, mRNA.
BC031272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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Best Local Similarity
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                          57
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/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue from day 20 and day 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG715343 472 bp mRNA linear EST 08-MAY-602677361F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4799726 5'
                                                                                                                                                                                                                                                                                                                                                                                                        GCACACGCTGCGCACCCGCAGCCGCGCTTCGTTGCTCATGATCGCGCTTCGCCCCGGGTGCC
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                                                                                                                                                                       Score 247.6; DB 12; Length 583;
Pred. No. 4.3e-35;
0; Mismatches 170; Indels 24;
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L Unpublished (1999)
Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMLOG89 row: j column: 15
High quality sequence stop: 470.
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/dome_lib="With MGC 96"
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1 (bases 1 to 472)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="IMAGE:4799726"
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BB628489 RIKEN full-length enriched, 16 days neonate cerebellum Mus musculus CDNA clone 9630009M09 5', mRNA sequence.
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I (bases 1 to 660)

Arakawa, T. Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,

Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,

Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,

Sonno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,

Sano, H., Sasaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K.,

Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,

Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTS (Arakawa, T., et al. 2001)

Contact: Yoshihide Hayashizaki
                           574 ATCCTGCGTGTCCGCGCCTTCCACCGCGTGCCACATAACTTGGTGGCCTCGACAGCCGTC 633
                                                                                                                         359 GGGCGACGTCGCTGCTGGCCCGGAGCCTGTGCCACGTGTGGATCTCCTTCGACGCCGGA 418
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                              693 GGGCGACGTTGGCAGCTAGGCAGGAGTCTGTGCCACGTGTGGATCTCCTTCGACGTGTAG 752
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
Itoh,M., Konno,H., Okazaki,Y., Muranatsu,M. and Hayashizaki,Y.
Normalization and subbraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               862 TCATGATCGCGATCACCTGGGCACTGTCCGCGCCTCATTGCTCTCGCCCGCTGCTTTAGG 921
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                                                                                    TCGGACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACC
Mus musculus (house mouse)
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Fax: 81-45-503-9216
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
                                                                           BI411238 929 bp mRNA linear EST 14-AUG-2001
602964578F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5120035 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not
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                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 929)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGTCCTGCCGGCCCG--AGGGCCGCCTTCTCTTCA-CGGTCCTGGTGGTGACG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   454 CTCATCTTGCCTGGTCCGCGAGCCTGAACTTCTCTGCTTTCACCTGTGCTTGTGGTGACT 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIGCTAGIGC -- TGCTGATCG - CIGCCACTITCCIGIGGAACCIGCTGGTTCCGGTCACC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      514 CTACTTGGTGTTTGCTGATCGTTTGCCACTTTCTTATGGAATCTGCTAGTTCTGGTGACT 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 ATCCCGCGGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 ATGGAGGCCGCTAGCCTTTCAGTGGCCACCGCCGTTGCCCTTGCCCTGGGACCCGAG 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM11292 row: 1 column: 20
High quality sequence start: 177
High quality sequence stop: 928.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
                                                                                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                  BI411238.1 GI:15172161
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BI411238
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Matches 421; Conserv
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                        RESULT 13
BI411238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 TrccGCATGGGCTCCAG--GAAGACCAACAGCGTCTCCCCCGTACCCGAAGCTGTGGAGG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGTGGTGTTTCACGGCACATTGCAAAGCA 862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 CTCATGGTGGGCATCCTCATCGGAGTGTTTGTGCTCTGCTGGTTCCCTTTCTTCGTCACA 289
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Alzawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
                                                                                                                                                    Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="RIKEN full-length enriched, 16 days neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TICCACCTGCCGCTTGGCGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 GAGCTCATCAGTCCCCTGTGTTCCTGGGACGTCCCTGCCATCTGGAAGAGCATCTTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               743 TITICGITITCGCCCGCCCGCCGGAGAGCTGTGCCGTTGCCGGCCACCATGCAGGTGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 4.3e-26;
0; Mismatches 131; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.2%; Score 198.4; DB 10; Length 660; 69.0%; Pred. No. 4.3e-26;
                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="cerebellum"
/dev_stage="16 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db xref="taxon:10090"
                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           /clone="9630009M09
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Best Local Similarity
Matches 319; Conserv
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Lark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Bddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Watter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Watterston, R. and Wilson, R. Unpublished (1998)

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L. Ontact: Stephen L. Johnson Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: zbrafish@watson.wustl.edu
Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution information can be found through the I.M.A.G.E.
Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: T7 from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Sugano SJD adult male"
//clone lib="Sugano SJD adult male"
//note="Vector: pME185-FL3; Site 1: DraIII (CACCATGTG);
//note="Vector: pME185-FL3; Site 1: DraIII (CACCATGTG);
//orbite local color (ATT CATGTGT (ATT CATTTTTTTTTTTTT);
//double-stranded cDNA was ligated to a DraIII adaptor
//grycogcorporggl, Algested and cloned into distinct DraIII
sites of the pME185-FL3 vector (5' site CACTGTGTG, 3' site
CACCATGTG). XhoI should be used to isolate the cDNA
                                                                                                                                                                                                              BM861710 655 bp mRNA linear EST 07-MAR-2002 fy49e02.xl Sugano SJD adult male Danio rerio cDNA clone IMAGE:5603043 3' similar to SW:5H5A_HUMAN P47898 5-HYROXYTRYPTAMINE SA RECEPTOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insert. Size selection was performed to exclude fragments <1.5kb. Library constructed and donated by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTRAAAGCTGCG and 3' end primer CGACCTGCAGCTGCA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 655)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 CCGCATAACTTGGTGGCCTCGACGCCGTCTCGGACGAACTAGTGGCAGCGCTGGCGATG
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1103 TACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAGATGA 1144
                                 410 TACAGCAGTGCTTTCAAGGTCTTCTTCTCCAAGGCAACAATGA 451
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/lab_host="DH10B (phage resistant)"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:5603043"
                                                                                                                                                                                                                                                                                                                                                                                    BM861710.1 GI:19229392
                                                                                                                                                                                                                                                                                                                                                                                                                                                Danio rerio (zebrafish)
Danio rerio
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JOURNAL
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KEYWORDS
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190 ATTG3 186	119	ପୁପ
749 TICGG 753	74	ò
O CTGCCTCTCTGTGTTGTGTTTGTCTACTGGAGATTTACAAAAGCTGCTAAGTTCCGT 191	250	Q
9 CTGCCGCTTGGCGTGGCCGTTTGTCTACGGAAGATCTACGAGGCGGCCAAGTTTCGT 748	689	δ
O GAGTGCCAGGTGAGCCAGGAGCCGTCTTACACCATCTTTCCACATTCGGGGCCTTCTAT 251	310	QQ
629 CGCTGCCAGGTGAGCCGGGAACCCTCCTATGCCGCCTTCTCCACCGGGGGCGCCTTCCAC 688	62	ò
7 GITATITGGCTCTGCCTCTGTITGGCTGGGGGTGAGACGTATTCGGAGGAGAACAIG 311	367	QQ
569 CTCATCGCCCTCGCGCTGCTCTTTGGCCGGGGCGAGGTGTGCGACGCTCGGCTCCAG 628	. 56	ð
427 CTAAAGACCCGGGAGAAGAAGATCTCCAATGTGATGATCGGGTTAACCTGGCTGCTTTCATCT 368	42	OD
509 CTGCGCACCGCAGCGCGCCTCGTTGCTCATGATCGCGCTCGCCGGGTGCCGTCGGCG 568	50	ò
487 AACGIGACCGCAAIAGCCCTTCGACCGTTACTGGTCCATAACTCGACACCTGGAGTACACC 428	4 8	qq
449 AACGIGGCGCCATCGCCCTGGGCCGCGACGGGCCATCACGCGCCACCTGCAGCACACG 508	44	ò
538 TGTCAAGTCTGGATATCGTTTGATGTCCTGTGCTGTACGGCTAGGATTTGG 488	53	qΩ
389 TGCCACGTGTGGATCTCCTTCGACGCCGGAGCCTGTCTGT	38	à
595 CCTCTCAGTCTGGTCCACGAGCTGAACGGCCGTCGGTGGGAGCTGGGTCGCGTTCTC 539	55	qu
329 CCACCGAGCCTGGCGAGCTGTCGACCGGCGACGTCGGCTGGTGGGCCGGAGCCTG 388	32	δ
655 CCCCACAACCTTGTAGCCTCCATGGCCATATCTGACGTCATGGTGGCAGCTTTGGTGATG 596	65	QQ

Search completed: September 7, 2004, 17:13:12 Job time: 2870 secs

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697, App
609, App
1, Appli
445, App
39, Appl
37, Appl
15, Appl
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Sequence 9, Appli
                                                                                                        7, 2004, 16:25:27; Search time 586 Seconds (without alignments) 9771.633 Million cell updates/sec
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                                                                                                                                                                                                       1152
1 cgccalggaggccgctagcc.....aagcagagatgaacacaggg 1152
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(gnz_6/ptodata/2/pubpna/US07 PUBCOMB seq:*
(cgnz_6/ptodata/2/pubpna/US06 FWF PUB.seq:*
(cgnz_6/ptodata/2/pubpna/US06 FWF PUB.seq:*
(cgnz_6/ptodata/2/pubpna/US06 FUBFOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-823-187-9

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US-10-313-946-34

US-10-311-671-25

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US-10-109-522A-1

US-10-109-52A-1

US-10-125-567A-445

US-10-345-680-3

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US-10-35-680-3

US-10-35-680-3

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                                                                                                                                                                                                                                                                                                                       3267054 segs, 2485319735 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                       - nucleic search, using sw model
                                                                                                                                                                                                                                                                IDENTITY NUC Gapoxt 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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Sequence 5, Applia Sequence 9467, Ap Sequence 2940, Ap Sequence 23167, A Sequence 21317, A Sequence 213298, Sequence 213298, Sequence 213299, Sequence 213299, Sequence 41, Applia Sequence 754, Applia Sequence 42, Appl Sequence 19, Appl Sequence 52, Appl Sequence 10, Appl Sequence 107, Ap Sequence 1, Appli Sequence 1, Appli Sequence 12, Appl Sequence 15, Appl Sequence 1, Appli Sequence 10, Appl Sequence 995, App Sequence 32, Appl Sequence 448, App US-10-029-386-9467 US-10-717-597-32 US-09-826-509-448 US-10-241-313-15 US-10-060-795B-1 US-10-060-795B-10 US-09-993-844-12 5636. 564. 4992.8 33082.8 3508.2 3508.2 3508.2 3508.2 3508.2 3608.3 3

ALIGNMENTS

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GENERAL LIVEMMILION:

GAPPLICANT: Grosse et al.

TITLE OF INVENTION: No. US2003019071SA1e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-157.

CURRENT APPLICATION NUMBER: US/09/976,782

CURRENT FILING DATE: 2001-10-12

FRIOR PILING DATE: 2000-10-16

FRIOR FILING DATE: 2000-10-16

FRIOR PILING DATE: 2000-10-16

FRIOR PILING
                                                                                                                          ; Sequence 15, Application US/09976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-976-782-15
RESULT 1
US-09-976-782-15
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Sequence

Sequence

Sequence

Sequence

OY 1021 CATCTGGAAAAGCATATTTCTGTGGCTACTCCAATTCTTCAACCCCCTGAT 1080 Db 1021 CATCTGGAAAAGCATATTTCTGTGGCTTGGCTACTCCTATTCTTCTAACCCCCTGAT 1080 OY 1081 TTACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCCCTTTACTTAACAAGA 1140 Db 1081 TTACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAG 1140 OY 1141 ATGAACACAGG 1152 Db 1141 ATGAACACAGG 1152 Db 1141 ATGAACACAGG 1152	-9 Application US/0982 No. US20030096952A1 ORMATION: Burgess, Catherine Gusev, Vladimir Y Liu, Xiaohong Majumder, Kumud Padigaru, Muralidh Patturajan, Meera	APPLICANT: Shinkets, Richard A APPLICANT: Spaderna, Steven K APPLICANT: Spytek, Kimberly APPLICANT: Taupier, Raymond J TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 15966-745; CURRENT APPLICATION NUMBER: 60/193,339 PRIOR FILING DATE: 2000-03-20 PRIOR PLING DATE: 2000-03-30 PRIOR APPLICATION NUMBER: 60/193,205 PRIOR PLING DATE: 2000-03-30 PRIOR FILING DATE: 2000-03-30	PRIOR APPLICATION NUMBER: 60/195,343	PRIOR APPLI PRIOR FILIN PRIOR FILIN NUMBER OF S SOFTWARE: P SEQ ID NO 9 LENGTH: 11 TYPE: DNA ORGANISM: PEATURE: NAME/KEY:	Ouery Match Query Match Best Local Similarity 97.7%; Pred. No. 2.9e-290; Matches 1125; Conservative 0; Mismatches 0; Indels 27; Gaps 3; Qy 1 CGCCATGGAGGCGTAGCTTTCAGTGGCCACGGCGGTTGCCCTTGCCTTGGACC 60 Db 20 CGCCATGGAGCCGTAGCTTTCAGTGGCCACGCGGGTTGCCCTTGCCTTGGACC 60 Qy 61 CGAGACCAGGAGCCGTAGCCTTTCAGTGGCCACGCGGGTTGCCCTTGCCTTGGACC 79 Qy 61 CGAGACCAGGAGCCGGACCCGAAGGCCCCAAGGCCCGAGGGGATTGCCCTGGGACC 79 [
Query Match 100.0%; Score 1152; DB 10; Length 1152; Best Local Similarity 100.0%; Pred. No. 7.2e-314; 1ndels 0; Gaps 0; Matches 1152; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy CCCATGGAGGCGGTAGCCTTTCAGTGGCCACCGCGGGGTTGCCCTGGGACC 60	Qy 121 GGGGGCGTCCTGCCGGGCCGAGGGCCGCCTTCTCTGTCTTCACGGTCCTGGTGGTC 180 Db 121 CGGCGCCGTCCTGCCGGGCCGAGGGCCGCCTTCTCTGTCTTCACGGTCCTGGTGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT	Qy 3.01 GGACGAACTAGTGGCAGCGCTGGCGAGCCTGGCGGAGTGGAGTTGCACCGG 3.60 Db 3.01 GGACGAACTAGTGGCAGCGTGGCGATGCCACCGAGCTGGCGGAGTGGAGTGCCCGG 3.60 Qy 3.61 GCGACGTCGGCTGGCCGGCTGGCCTGTGGATCTCCTTCGACGCGGAGC 4.20 Db 3.61 GCGACGTCGGCTGGCCTGTGCCCACGTGTGGATCTCCTTCGACGCCGGAGC 4.20 Qy 4.21 CTGTTGTGCTGCCCCGGCGCGCTCGGGAACGTGGCGCATCGCCCTGGGCCGACGG 4.80 Db 4.21 CTGTTGTGCTGCCCCCGCCGCGCCTCGGGAACGTGGCCATCGCCCTGGGCCGACGG 4.80 A2.1 CTGTTGTGCTGCCCCCGCCGCGCCTCGGGAACGTGGCGGCCATCGCCCTGGGCCGACGG 4.80	QY 481 GGCCATCACGGCACCTGCAGCACCCGCACCCGCAGCCGCACCTGTTGCTCAT 540 B	661 CGCCTTCTCCACCCGGGGCGCCTTCCACCGGCTTGGCGTGGTGCCGTTTGTCTACCG [0.0 0.0

CGAGACCAGCAG-----CGGGACCCCAAGCCCGAGAGGGATACTCGGTTCGACCCCGAG 133

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                                                                                                                                                                                                   APPLICANT: Buses, Catherine
APPLICANT: Gusev, Viadamir Y
APPLICANT: Gusev, Viadamir Y
APPLICANT: Liu, Xiaohong
APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Patturajan, Meera
APPLICANT: Spaderna, Steven
APPLICANT: Spaderna, Steven
APPLICANT: Spaderna, Steven
APPLICANT: Spaderna, Steven
APPLICANT: Spatek, Kimberly
APPLICANT: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE OF INVENTION NUMBER: 60/193, 205
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-11
PRIOR PRILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/195, 525
PRIOR PRILING DATE: 2000-04-11
PRIOR PRILING DATE: 2000-04-11
PRIOR PRILING DATE: 2000-04-11
PRIOR PRILING DATE: 2000-04-14
PRIOR PRILING DATE: 2000-04-14
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PRIOR PRILING DATE: 2000-0
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Best Local Similarity 97.5%; Pred. No. 2.3e-289;
Matches 1123; Conservative 0; Mismatches 2;
                                                                                Sequence 11, Application US/09823187
Publication No. US20030096952A1
GENERAL INFORMATION:
                                                                                                                                                                                   APPLICANT: Burgess, Catherine APPLICANT: Gusev, Vladimir Y APPLICANT: Liu, Xiaohong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023252A1 7476053CB1
US-10-333-946-34
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APPLICANT: RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R. APPLICANT: KALLICK, Deborah A.; CHAWLA, Narinder K. APPLICANT: HAFALIA, APPLI J.A.; YAO, Monique G. APPLICANT: HAFALIA, APPLI J.A.; YAO, Monique G. APPLICANT: LU, Yan; TRIBOULEY, Catherine M. APPLICANT: LU, Yan; TRIBOULEY, Catherine M. APPLICANT: GRAUL, Richard C.; WARREN, Bridget A. TILE, ETHERICANT: LEE, ETHERINE COUPLED RECEPTORS FILE REFERENCE: PI-0176 USN
CURRENT APPLICATION NUMBER: US/10/33,946
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/221,478
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 2000-08-3
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-13
PRIOR PRIOR FILING DATE: 2000-09-13
PRIOR FILING DATE: 2000-09-13
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PRIOR PRI
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Pred. No. 4.2e-289;
0; Mismatches 0;
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Best Local Similarity 97.6%;
Matches 1121; Conservative
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Sequence 34, Application US/10333946
Publication No. US20040023252A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael
APPLICANT: RAVIZU, Chandra S.; LAL, Preeti G.
APPLICANT: BURFORD, Neil; YUE, Henry
APPLICANT: GANDHI, Ameena R.; ELLIOTT, Vicki S.

RESULT 4 US-10-333-946-34

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61 ACCAGCAG-----CGGGACCCCAAGCCCGAGGGATACTCGGTTCGACCCCGAGGGGC 114
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                                                 APPLICANT: HENNANDEZ, Roberto
APPLICANT: HENNANDEZ, Roberto
APPLICANT: HENNANDEZ, Roberto
APPLICANT: BOROWSKY, Mark L.
APPLICANT: THORNTON, Michael B.
APPLICANT: THORNTON, Michael B.
APPLICANT: HE Ann
TITLE OF INVENTION: G-PROTEIN COUDLED RECEPTORS
TITLE OF INVENTION: G-PROTEIN COUDLED RECEPTORS
TITLE OF INVENTION: G-PROTEIN COUDLED RECEPTORS
TITLE OF INVENTION: G-PROTEIN OF 12.03
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212, 483
PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/215, 209
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/218, 936
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/218, 936
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-15
PRIOR APPLICATION NUMBER: 60/219, 154
PRIOR FILING DATE: 2000-07-15
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7474977CB1
RAMKUMAR, Jayalaxmi
AU-YOUNG, Janice K.
ELLIOTT, Vicki S.
HERNANDEZ, Roberto
WALEH, Roderick T.
BOROWSKY, Mark I.
THORNTON, Michael B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 1114; Conserv
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                                           ATCACACGGCACCTGCAGCACACGCTGCGCACCCGCAGCCGCGCCTCGTTGCTCATGATC 525
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Publication No. US20040072996A1
GENERAL INFORMATION:
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TRIBOULEY, Catherine M.
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APPLICANT: LAL, Preeti G.
APPLICANT: HARALIA, Mariah R.
APPLICANT: HARALIA, April J. A.
APPLICANT: GANDHI, Ameena R.
APPLICANT: GANDHI, Meena R.
APPLICANT: GANDHI, Meena R.
APPLICANT: GANLICK, Deborah A.
APPLICANT: GRIFFIN, Jennifer A.
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CHAWLA, Narinder K.
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ARVIZU, Chandra S.
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YAO, Monique G.
YANG, Junming
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KHAN, Farr
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Pred. No. 2.4e-202;
0; Mismatches 13; Indels 26;
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Best Local Similarity 95.4%;
Matches 810; Conservative
                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: (2218)..(2886)
US-10-017-161-697
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; Publication No. US20030143668A1
; Fublication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ARIYAMA, YUTAKA
; APPLICANT: ARIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TILLE OF INVENTION: NOVEL G PROTEIN-COUPLED REC
; FILE OF INVENTION: NOVEL G PROTEIN-COUPLED REC
; FILE OF INVENTION: NOVER: US/10/017,161
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOGTWARE: PatentIn Ver. 2.1
; SEQ ID NO 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION: TRANSCENIC MICE CONTAINING 5-HTSB
TITLE OF INVENTION: SEROTONIN RECEPTOR GENE DISRUPTIONS
TITLE OF INVENTION: SEROTONIN RECEPTOR GENE DISRUPTIONS
TITLE OF INVENTION: 2002-03-28
CURRENT APPLICATION NUMBER: US 60/280,553
PRIOR FILING DATE: 2001-03-29
NUMBER: OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 732.8; DB 15; Length Pred. No. 8.2e-196; O; Mismatches 202; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/10109532A; Publication No. US20030009780A1; GENERAL INFORMATION:
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79.98;
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Best Local Similarity
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publication No. US2003035833A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: AAFLY KIYOSHI
APPLICANT: AAFLICANT: AAFLY KIYOSHI
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFREENCE: 084335/166
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR PLILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PATENT NOS: 2070
SOFTWARE: PATENT NOS: 2010
SOFTWARE: PATENT NOS: 2010
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Matches 810; Conserv
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US-10-292-798-609
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PROTEIN-COUPLED RECEPTORS

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APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Burmer, Glenna C.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROJ
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/257,144
NUMBER: OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 445

LENGHI: 1074
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Pred. No. 1.1e-129;
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US-10-225-567A-445; Sequence 445, Application US/10225567A; Publication No. US20030113798A1; GENERAL INFORMATION:

APPLICANT: LifeSpan Biosciences

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PUBLICARY: Willennium Pharmaceuticals, Inc.
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
MAPLICANT: Weinstewariu, Karichel, Inc.
APPLICANT: Venkateswariu, Karichel, Inc.
APPLICANT: Venkateswariu, Karichel, Inc.
APPLICANT: Venkateswariu, Karichel, Inc.
TITLE OF INVENTION: WENFOOS APPL COMPOSITIONS FOR TREATING
ITTLE OF INVENTION: WENFOOS APPL CANDON ACCOUNTY ASS, 559, 34021, 44099, 25278,
ITTLE OF INVENTION: WENGOGIAL DISORBERS USING 1435, 559, 34021, 44099, 25278,
ITTLE OF INVENTION: WENGOGIAL DISORBERS USING 13601, 18926, 318, 2058 OR 6351 MOLECULES.
ITTLE OF INVENTION: WENGOGIAL DISORBERS USING 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
ITTLE OF INVENTION: WORDER: US 60/349,511
PRIOR APPLICATION WORBER: US 60/349,511
PRIOR APPLICATION WUMBER: US 60/365,041
PRIOR APPLICATION WUMBER: US 60/365,041
PRIOR FILING DATE: 2002-04-18
PRIOR FILING DATE: 2002-04-18
PRIOR PRILING DATE: 2002-01-26
PRIOR PRILING DATE: 2002-01-26
PRIOR PRILING DATE: 2002-11-05
PRIOR PRILING DAT
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                                                                                                                                                                                                                                                                      Length 1074;
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Pred. No. 1.1e-129;
0; Mismatches 279; I
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Best Local Similarity
Matches 729; Conserv
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US-10-345-680-39
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SAPLICANT: Milennium Pharmaceuticals Inc.
APPLICANT: Milennium Pharmaceuticals Inc.
APPLICANT: Garcoll, Joseph M.
APPLICANT: Garcoll, Joseph M.
APPLICANT: Garcoll, Joseph M.
APPLICANT: Healy, Aileen
APPLICANT: Healy, Aileen
APPLICANT: Weich, Nadine S.
APPLICANT: Weich, Nadine S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: 15513, 17622, 302, 5677, 194, 14393, 28059, 7366, 12212,
TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
TITLE OF INVENTION: 15513, 17622, 684A
TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
FILE REFERENCE: MPIO2-019PIRNOMNIM
CURRENT APPLICATION NUMBER: US 60/354,333
PRIOR APPLICATION NUMBER: US 60/360,258
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-16
PRIOR FILING DATE: 2002-04-26
PRIOR FILING DATE: 2002-06-06
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US-10-352-684A-15
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                                                                                                                                34021, 44099, 25278,
62553, 302, 323,
2058 OR 6351 MOLECULES.
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Pred. No. 1.1e-129;
0; Mismatches 279; Indels 24;
        APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Venkateswarlu, Karichtei
TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: WETHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2056
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2056
FILE REFERENCE: MPIO2-012PIRNM OMNI
CURRENT APPLICATION NUMBER: US 60/349,511
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-02-18
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-15
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-08-14
PRIOR FILING DATE: 2002-08-17
PRIOR PLING DATE: 2002-10-21
PRIOR PLING DATE: 2002-10-26
PRIOR PLING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 66
SOFTWARKE: FRASERE FOR WINGOWS VERSION 4.0
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Best Local Similarity 70.6%;
Matches 729; Conservative (
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US-10-345-680-37
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ORGANISM: Homo Sapiens
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NAME/KEY: CDS
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LENGTH: 1159
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APPLICANT: Clark, Hilary
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kilary
APPLICANT: Fechtel, Kilary
APPLICANT: Howes, Steven H.
APPLICANT: Howes, Steven H.
APPLICANT: Reshick, Richard J.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graham, James R.
APPLICANT: Graperics Institute, Inc.
TITLE OF INVENTION: POLYNOCIEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6401
CURRENT APPLICATION NUMBER: US/09/823,245A
CURRENT FILING DATE: 2001-03-29
PRIOR FILING DATE: 2000-04-06
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GAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGACTCC
                                                                                                                            TGGCGGGAGCAGAAGGAGGCGAGCCATGATGGTGGGAATTCTGATTGGCGTGTTT
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43.1%; Score 496; DB 13;
Best Local Similarity 70.5%; Pred. No. 4.1e-129;
Matches 728; Conservative 0; Mismatches 280;
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US-09-823-245A-617
Sequence 617, Application US/09823245A
Publication No. US20020039760A1
GENERAL INFORMATION:
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US-09-823-245A-617
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LENGTH: 2700
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Pred. No. 1.1e-129;
0; Mismatches 279; Indels 24;
   PRIOR FILING DATE: 2002-06-24

PRIOR APPLICATION NUMBER: US 60/392,480

PRIOR PILING DATE: 2002-06-29

PRIOR APPLICATION NUMBER: US 60/394,128

PRIOR FILING DATE: 2002-07-03

PRIOR FILING DATE: 2002-07-31

PRIOR FILING DATE: 2002-07-31

PRIOR FILING DATE: 2002-09-13

PRIOR FILING DATE: 2002-09-13

PRIOR PILING DATE: 2002-09-13

PRIOR PILING DATE: 2002-09-13

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NUMBER OF SEQ ID NOS: 62

LENGTH: 1159
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Best Local Similarity 70.6%;
Matches 729; Conservative 0
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; LOCATION: (64)
US-10-352-684A-15
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                                                                                                                                                           DB 11; Length 1074;
                                                                                                                                                                                              Indels
                                                                                                                                                         ch 42.8%; Score 492.8; DB 11; Il Similarity 70.3%; Pred. No. 2.4e-128; 726; Conservative 0; Mismatches 282;
     PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFFWARE: Patentin Version 2.1
SEQ ID NO 446
                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                        US-09-826-509-446
                                                                      LENGTH: 1074
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Publication No. US20030204073A1
GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TILLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
TILLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: AREN-207
CURRENT APPLICATION WINBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR APPLICATION NUMBER: 09/170,496
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Search completed: September 7, 2004, 18:33:10 Job time : 592 secs
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GenCore version 5.1.6
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	September 7, 2004, 14:14:17 ; Search time 4454 Seconds (without alignments) 11210.412 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-976-782-15 1152 1 cgccatggaggccgctagccaagcagagatgaacacaggg 1152
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	3470272 segs, 21671516995 residues

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

6940544

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

1: 9b ba: *
2: 9b htg: *
3: 9b in: *
4: 9b om: *
5: 9b pat: *
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score Match Le Match	1		عد ا			SUMMARIES		
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AX527761	VERSION	AX52	7761.1		1722	R4		

1 Grosse, W.M., Alsobrook, J.P., Lepley, D.M., Burgess, C.E., Mishra, V., Kekuda, R., Li, L., Padigaru, M., Shimkets, R.A., Zerhusen, B.D., Spytek, K.A., Edinger, S., Gerlach, V., Macdougall, J., Stone, D., Homo sapiens Homo sapiens Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Novel proteins and nucleic acids encoding Patent: WO 0174851-A 9 11-OCT-2001;
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Pred. No. 2.7e-168;
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Pred. No. 2.7e-182;
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Patent: WO 0230974-A 15 18-APR-2002,
Curagen Corporation (US)
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Above Angle Angl	785 CCACCATGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
481 GGCCATCACACACACACACACACACACACACACACACACA	REFERENCE Nammalia; Eutheria; Primates; Catarrinni; Hominidae; Homo. RUTHORS Thornton,M., Patterson,C., Lal,P., Burford,N., Yue,H., Gandhi,A.R., BIliot,V.S., Ramkumar,J., Baughn,M.R., Kallick,D.A., Walia,N.K., Hafalia,A.J., Yao,M.G., Lu,Y., Tribouley,C.M., Policky,J.L., Kearney,L., Graul,R.C., Warren,B.A. and Ding,L. TITLE G-Protein coupled receptors JOURNAL Patent: WO 0210387-A 34 07-FEB-2002; Incyte Genomics, Inc. (US) FEATURES Location/Qualifiers /mol_type="unassigned DNA"

355 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	0	1000 TGGAAAAGCATATTCTGTGGCTTTGTTCTTCTTCTTCTTCAGCCCCTGATTTAC 1085 ACAGCTTTTAACAAGAACTACAACAACTCCAATTCTTTCT	SOURCE Unidentified ORGANISM unidentified Unclassified. **REFERENCE 1 AUTHORS Mishray.C.**, Spytek.K.A.*, Taupier.R.J.*, Vernet,C.A.*, Colman,S.D.*, AUTHORS Mishray.M.*, Patturajan,M.*, Burgess,C.E.*, Smithson,G.*, Tichernev.V.T.*, Padigaru,M.*, Patturajan,M.*, Burgess,C.E.*, Smithson,G.*, Millet,I.*, Peyman,J.A.*, Stone,D.*, Gunther,E.* and Ellerman,K.* TITLE Human polymotleotides and polypeptides encoded thereby JOURNAL Pattent: WO 022473-A 29 28-MAR-2002; Curagen Corporation (US) Location/Qualifiers Source 1.1155
	linea linea ertebra Homini, ,D.B., (F.A., P. F.A., P. Total	State Matches 1114; Conservative 97.7%; Pred. 100. 5.9e-167; Matches 1114; Conservative 97.7%; Pred. 100. 5.9e-167; Indels 21; Gaps 3; Matches 1114; Conservative 0; Mismatches 5; Indels 21; Gaps 3; Qy S ATGAAGGCGCTACCCTTCCCTTGCCCTGGACCCGAG 4	Qy 185 CTAGTGCTGCTATTCCTGTGGAACCTGCTGGTCACCATCCCG 244 Db 175 CTAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTTCCGGTCACCATCCCG 234 Qy 245 CGGGTCCGTGCTCCACCGCTTCCTGTGGTGCTCTCGGTCTCGGAC 334 Db 235 CGGGTCCGTGCTCCACCGCTGCCGCATAACTTGGTGGCCTCCGACGGCGTCTCGGAC 294 Qy 305 GAACTAGTGGCACCGCTGCCGCATAACTTGGTGGCCTCGACGGCGTCTCGACG 294 Qy 305 GAACTAGTGGCAGCGCTGCCACCACGAGCCTGGCGAGTGACCTGGACGGGGA 364 Db 295 GAACTAGTGGCAGCTGGCGATGCCACCGAGCTGGCGGAGTGACCTGGACCGGGCA 354 Qy 365 CGTCGGCTGTGCCGAGCCTGTGCCACCGAGCCTGGCGAGTGACCTGGACCGGGCA 354 Qy 365 CGTCGGCTGTGCCACGTGCCACCGAGCCTGGCCACTTCGACCGGGCA 354 Qy 365 CGTCGGCTGTGCCACCTGCCACCGAGCCTGGCCACTTCGACCGGGCA 354 Qy 365 CGTCGGCTGCTGCCACCTGCCACCGAGCCTTCGACCGGAGCCTGT 424

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/db_xref="taxon:32644" /note="Description of Unknown Organism: NOVX Nucleic Acid" ORIGIN Query Match 88.2%; Score 1016; DB 6; Length 1155; Best Local Similarity 97.2%; Pred. No. 1.3e-159; Matches 1087; Conservative 0; Mismatches 0; Indels 31; Gaps 4; Oy 36 CCGCGTTGCCTTGCCTTGGGACCCGAGCCGGACCCGAGCCGGACCCGAGCCG 94 Dh. 68 CCGGCTTGCCTTGGGACCCGAGCAGCAGCAGCAGCAGCACCCGAACCCG 127	95 128 155 188 215		GGGCCATGGCCTGGGCGGACGGGCCATCACACGGCCCTGCAGCACGCGCGCG	Db 650 CAGGTGAGCCGGGAACCCTCCTATGCCGCCTTCTCCACCTGCGGGCGCTTCCACCTGCGG 709 Qy 695 CTTGGCGTGGTGCTTTGTCTACCGGAAGATCTACGAGGCGCCCAAGTTTCGTTTCGGC 754 Db 710 CTTGGCGTGGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGCCCAAGTTTCGTTTCGGC 769 Qy 755 CGCCGCCGGAAGACTTGTCTACCGGAAGATCTACGAGGCGCCCAAGTTTCGTTTCGGC 769 Qy 756 CGCCGCCGGAAGACTGCCGTTGCCGTTGCCAAGTTGCAAGTTCGTTTCGGC 769 Db 770 CGCCGCCGGAAGACTGCCGTTGCCGTTGCCAAGTTGCAAGGTGACGTGTCCTTC 874 B15 GAAGCACCTGATGAGGCTGTGTGTTCACGGCACATTGCAAAGCAACGGTGTCCTTC 877 Qy 875 CAGGTGAGCGGGACTCCTGGCGGAGCAGTGCGAATTGCAAAGCAACGGTGTCCTTC 877 Qy 875 CAGGTGAGCGGGGACTCCTGGCGGAGCAGAATTGCAAAGCAACGGTGTCCTTC 877 Qy 876 CAGGTGAGCGGGACTCCTGGCGGAGCAGAAGCAATTGCAAAGCAACGATGTGGGA 937 Qy 877 CAGGTGAGCGGGGACTCCTGGCGGGAGCAGAGCGAGCACTGATGGTGGGA 937 Qy 878 CAGGTGAGCGGGGACTCCTGGCGGGAGCAGCAGCAGCACTGATGCTGGA 937 Qy 878 CAGGTGAGCGGGGACTCCTGGCGGAGCAGCAGCAGCACTCATCCTGACGGAACTCATCAGCG 994 Qy 878 CAGGTGACCGGGGACTCCTGGAGCAGAGGCGACCACTGACGCAGCACTCATCAGCGGA 937 Qy 878 CAGGTGAGCGGGGACTCCTGGAGCAGAGGCGACCACTGACGCACACTCAGCGGAACTCATCAGCG 994 Qy 879 CCACTCTGATGGCGTGCTTGCTGGAACCCCTTCTTCCTGGACGCAACTCATCAGC 997 Qy 995 CCACTCTGTGCCTGCCCCCCCCCCTTCTGGAAAACCTTTCTGTGGCTTTCATCTGGGCTAC 1054

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from the whole human genome sequences using our automated
              system that contains programs of gene finding (GeneDecoder), sequence search, motif-domain assignment and transmembrane helix prediction.

And the sequence is submitted by the collaborative project between [Computational Biology Research Center (CBRC), National Institute of Advanced Industrial Science and Technology (AIST) and [Genome Science Division, Research Center for Advanced Science and Technology (RCAST), University of Tokyo).
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/evidence=not_experimental
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/organism="Homo sapiens"
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Direct Submission

Submitted (11-JUL-2001) Makiko Suwa, Computational Biology Research
Center (CBRC), National Institute of Advanced Industrial Science
and Technology (AIST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan
(E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/,
Tel:81-3-3599-8080, Fax:81-3-3599-8081)
This sequence is a seven transmembrane helix receptor candidate
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Muctot Submission
Submitted (07-OCT-2000) Department of Genetics, Mashington
Submitted (07-OCT-2000) Department of Genetics, Missouri 63108, USA
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Oct 7, 2000 this sequence version replaced gi:9454621.
                                                                                                                                                                                                                                                                                            PRI 07-0CT-2000
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Direct Submitssion
Submitted (21-AUG-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (Dases 1 to 112883)
Waterston, R.H.
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Submitted (26-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MD 63108, USA
5 (bases 1 to 112883)
                                                                                               976
                                                                           814
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                    CTIGGCGIGGIGCCGTITGICIACCGGAAGAICTACGAGGCGGCCAAGITICGTITCGGC
                                                                           CGCCGCCGGAGAGCTGTGCTGCCGTTGCCGGCCACCATGCAGGTGAGGTCCAAGGTAAAG
                                                                                                                                                                                                                                                                            ACCO09404 112883 bp DNA linear PRI 07-O
Homo sapiens BAC clone RP11-28H22 from 2, complete sequence.
ACCO09404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 112883)
Sulston, J. E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu ------ Summary Statistics

Center code: WUGSC

Center project name: H_NH0028H22

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatanes, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are polymorphic base pair differences in the overlaps between the clones RPI1-425F6, RPI1-28H22, and RPI1-425F6. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NID:g3235608) ub04e12.rl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence RP11-28H22 contains imperfect dinucleotide (CT and GC repeats from base position 53407 to 53507. The region is covered by a single clone, the fidelity of the sequence cannot be guaranteed. The length of sequence is consistent with PCR from clone DNA, and corresponds to restriction digest information: hindIII band size 5664 in silico, and 5694 real.
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. L MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                              overlap;
                                                                                                                                                                                                                                                                                                                                                                                       The clone sequenced to the left is RPI1-425F6, 200 bp overlap clone sequenced to the right is RPI1-98C1, 200 bp overlap. A start of this clone is at base position 157644 of RPI1-425F6; actual end is at base position 21685 of RPI1-98C1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NID:97855185)"
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/...101
/hote="similar to EST AW069620 (NID:g6024618)
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NEIGHBORING SEQUENCE INFORMATION:
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
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1062. .1194
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/rpt_family="MER1_type"
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/note="similar to
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/note="similar to
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/note="similar to
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/note="similar to
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Qy 1 CGCCATGGAGGCCGCTAGCCTTTCAGTGGCCACCGCCGGCGTTGCCCTTGCCCTGGGACC 60	Qy 61 CGAGACCAGCAGCAGGGGGGGACCCCAAGCCCGAGGGGTACTCGGTTCGACCCCGA 119	Db 41856 CGAGACCAGCAGCAGCACCCGAGCCCCAAGCCCGAGGGGATACTCGGTTCGACCCCGA 41915	Qy 120 GCGGCGGCGTCCTGCCGGGCCGAGGGCCGCCCTTCTCTCTTCACGGTCCTGGTGGTGA 179	Db 41916 GCGGCCCTCCTGCCGGGCCGAGGCCGCCCTTCTCTGTCTTCACGGTCCTGGTGGTGA 41975	Qy 180 CGCTGCTAGTGCTGATCGCTGCCACTTTCCTGTGGAACCTGGGTCGCGTCACCA 239	Db 41976 CGCTGCTAGTGCTGCTGCTGCCTGCCTTTCCTGTGGAACCTGCTTCCGGTCCGGTACGCTACCACTTTCCTGTGGAACCTGCTTCCTGCTAGAACCTGCTAGAACCTGCTAGAACCTGCTAGAACCTGCTAGAACCTGCTAGAACCTGCTAGAACGTAGAACGTAGAACGAAC	Qy 240 TCCGGGGGGCGGTGCCTTCCACGCGGTGCGGATAACTTGGTGGCGCCTCGACGGCGGTCT 299	Db 42036 TCCCGCGGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGGCGTCT 42095	Qy 300 CGGACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCTGGCGAGTGAGCTGTCGACCG 359	Db 42096 CGGACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGATGAGCTGTCGACCG 42155	Qy 360 GGCGACGTGGCTGCTGGGCCGGAGCCTGTGCCACGTGTGGATCTCCTTCGACGCGGGGG 419	Db 42156 GGCGACGTCGGCTGGCCGGAGCCTGTGCCACGTGTGGATCTCCTTCGACGCCGGAG 42215	Qy 420 CCTGT	Db 42216 CCTGTGCCACGTGTGGATCTCCTTCCACGGCTGTGCCCCGCCGGCCTGGGGAACGTG 42275	Qy 455 GCGGCCATCGCCCTGGGCCGCGACGGGGCCATCACGCGCACCTGCAGCACACGCTGCGC 514	Db 42276 GGGGCCATCGCCCTGGGCCGCGAGGGCCCATCACACGGCACCTGCAGCACGCTGCGC 42335	Qy 515 ACCGGGGCGCGCCTCGTTGCTCATGATCGCGCCGGGGGGGG	Db 42336 ACCGCGGGCCTCGTTGCTCATGATCGCGCTCGCCGGGTGCCGTCGGCGCTCATC 42395	Qy: 575 GCCTCGCGCTGCTCTTTGGCCGGGGGGAGTGTGCGACGCTCGGCTCCAGCGCTGC 634	Db 42396 GCCCTCGCGCCGCTGCTCTTTGGCCGGGGCGAGGTGTGCGACGCTCGGCTCCAGCGCTGC 42455	Qy 635 CAGGIGAGCCGGGAACCTCCTAIGCCGCCTTCTCCACCGGGGCCTTCCACCGGGG	Db 42456 CAGGTGAGCCGGGAACCCTCTATGCCGCCTTCTCCACCCGCGGCGCCTTCTCCACCTGCCG 42515	Qy 695 CTTGGCGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCCAAGTTTCGTTTCGGC 754	Db 42516 CTTGGCGTGGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCCAAGTTTCGTTTCGC 42575	Qy 755 CGCCGCCGGAGAGCTGTGCTGCCGTTGCCGCCACCATGCAGGTCCAAGGTAAAG 814	Db 42576 CGCCGCGGAGAGCTGTGCTGCCGTTGCCGGCCACCATGCAGGTGAGGGTGGGCTGAGG 42635	Qy 815 GAAGCACCT 823	Db 42636 AACGITGCI 42644	יו היווסקס	2002; L KWG 24 00 00 1	DEFINITION Home sapiens clone RP11-13G16, *** SEQUENCING IN PROGRESS ***, 55	ACCESSION AC011638.3 GI:7137674	HTG: HTGS PHASE1.
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CCTATGCCGCCTTCTCCACCCGCGCGCCTTCCACCTGCCG 694 TGCCGTTGCCGGCCACCATGCAGGTGAGGGTGGGCTGAGG 42635 184328 bp DNA linear HTG 01-MAR-2000 11-13G16, *** SEQUENCING IN PROGRESS ***, 55 TIGCCGTTGCCGGCCACCATGCAGGTGAGGTCCAAGGTAAAG 814 Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; SOURCE ORGANISM

> 26; Gaps Length 112883; Score 756.2; DB 9; Length Pred. No. 1e-116; 0; Mismatches 13; Indels Unery Matcn Best Local Similarity 95.4%; Matches 810; Conservative

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f 100 bp
g of 2736 bp in length
f 100 bp
g of 3402 bp in length
f 100 bp
g of 776 bp in length
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1999)
http://ftp.genome.washington.edu/RM/RepeatMasker:html
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    Eutheria; Primates; Catarrhini; Hominidae; Homo
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------ Project Information
Center project name: L3324
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-13G16
Unpublished
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COMMENT

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Other publication FR 2701265 940812
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                                                                                                                                                                                                                                                                                      Length 977;
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                      Score 745; DB 9; Lt
Pred. No. 1.9e-114;
0; Mismatches 20;
                                                     /codon_start=1
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/number=1
/pseudo</pre>
    gene="5-HT5B"
                                                                                                                                                                                                                                                                                        tch 64.7%;
al Similarity 94.6%;
803; Conservative
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/ translation="MEVSNLSGATPGILAFPPGPESCSDSPSSGRSMGSTPGGLILPGR
BPPESAFTULVULIANLILAATENWILLULVITIENRAAFFWPDHILASTAVSDVLVA
VLVWPLISLVSELSGASTRWGIGRSLCHVWISPDYLCCTASIWNVAAIALDERWTITHEL
OYTLETERSRASALMIAITWALSALIALAPLLFGWGBAYDARLORCGVSGEPSYAVFST
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ATVTPGTSGDSWREGOKERRAAMWGILIGVPULCWIPFELTELISPLGACSLPPIWKS
IFLWIGYSNSFPNPLIYTAFNKNYNNAFKSLFTKQR"
Matthes, H.

Direct Submission
Submitted (28-DEC-1992) H. Matthes, Laboratoire de Genetique
Submitted (28-DEC-1992) H. Departement de Neurobiologie, 11 rue
Humann, F-67000 Strasbourg, FRANCE
Location/Qualifiers
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Pred. No. 1.8e-112;
0; Mismatches 202;
                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAA49501.1"
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/db_xref="SWISS-PROT:P31387"
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/tissue type="brain"
15. 2055
                                                                                                                                                                                                                                                                                                  312. .1424
/codon_start=1
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/label=exon2
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/label=exon1
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911; Conserv
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Matthes, H., Boschert, U., Amlaiky, N., Grailhe, R., Plassat, J.L., Muscatelli, F., Mattei, M.G. and Hen, R.

Mouse 5-hydroxytryptamine5A and 5-hydroxytryptamine5B receptors define a new family of serotomin receptors: cloning, functional expression, and chromosomal localization

Mol. Pharmacol. 43 (3), 313-319 (1993)
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5-HT5B serotonin receptor.
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Mus musculus
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QY 545 GCGCTCGCCCGGGTGCCGTCGATCGCCTCGCGCCCTGCTCTTTGCCCGGGGC 604 Db 837 GCGATCACCTGGCCACTGTCGCCCCGCTGCTCTTTTGGCTGGGGC 896 Cb 605 GAGGTGCGACCTGGCCAGGTGACCCGGGGAACCCTCTATGCCGCGC 664 Cp 605 GAGGTGCGACCTCGAGCTGCCAGGTGACCGGGGAACCCTCTATGCCGCGC 664 Cp 605 GAGGTGTCCGACCTCGAGGTGCCAGGTGACCCTCTATGCCAGGTGCCTCTATGCCAGGTGCCTCTATGCCAGGTGCCTTTACCAGGAGCCTCCTATGCCAGGTGCCGTTGCCAGGTGCCGTTTGCTACCGGAAG Qy 665 TTCTCCACCCGGCGTTCCACCTGCCGCTTGGCGTGGTGCCGTTTGTCTACCGGAAG	957 TTCTCCACCTGCGAGCCTTCTACCTCTCTGGGTGCTCTTCGTCTGGAAA 725 ATCTACGAGGCGGCCAAGTTTCGTTTCGCCGCCGCCGAGAAGTTGCTGCGTTGCCG 726 ATCTACGAGGCGCCAAGTTTCGTTTCGTTTCGCCGCCGCGAGAGCTGTGCTGCTGTTGCGTTGCCG 1017 ATTACAAGCCGCCAAGTTTCGTTTCGTTCGGTCGCGGCGGGGGGGG	785 GCCACCATGCAGGTCAAGGTAAGGAAGCCTGATGAGGTGAGGTTGCTTC 10.77 GCCACCACGCAGGCAAAGGAAGCACCTCCGGAGTCTGAGGTGGTTC 845 ACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGGGTGTGTTC 816	1185 AACCAGATACGGGAACCATCATCATCACCACTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	1085 ACAGCTTTTAACAAGAACTACAACAACTACAAGAGCTCTTTACTAAGGAGAGATGA 1365 ACTGCCTTTAATAAGAATTACAACAAGGCCTTCTAAGAGCTCTTTACTAAGGAGATGA 1365 ACTGCCTTTAATAAGAATTACAACAATGCCTTCAAGAGCTCTTTACTAAGCAGATAAA 1365 ACTGCCTTTAATAAGAATTACAACAATGCCTTCAAGAGCTCTTTACTAAGCAGATAA 1365 ACTGCCTTTAATAAGAATTACAACAATGCCTTCAAGAGCTCTTTACTAAGCAGATAA 186627 1000 AR080627	S	Query Match 63.4%; Score 729.8; DB 6; Length 2226; Best Local Similarity 79.6%; Pred. No. 5.5e-112; Indels 27; Gaps 3; Qy 3 CCATGGAGGCGGTTAGCCTTTCAGGGCACCCGGGGTTGCCCTTGCCTGGGACCCG 62 Db 301 CAATGGAGGCCGTAGCCTTCAGGCGCACCCCTGGCATTGCTTTCTCCGGGACCCG 360 Qy 63 AGACTGCAGCAGCCCCCAAGCCCGAGGGATTCGGTTGCTTTCTCGGGAGCC 360 Qy 63 AGACTGCAGCAGCCCCCAAGCCCGAGGGATTCCGGTAGGTTCCGTTGGTTCGATCGCCCCAGGGG 122 Db 361 AGACTGCAGTGACCCCAAGTTCCGGCAGAAGCATGGGATCCACCCCAGGGG 414

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Search completed: September
Job time : 4463 secs
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GRFYVPLAVVLFVYWKIYXYARKFRFGRRRRAVVPLPATTQAKEAPQESETVFTARCR
ATVAFQTSGDSWREGKERRAMWYGTLIGVPVLCWIPFFLTELVSPLCACSLPPIWKS
IFFWLGYSNSFFNPLIYTAFNKNYNNAFKSLFTKQR"
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mRNA, 5'
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EPPFSAFTVLVVTLLVLLIAATFLWNLLVLVTILRVRAFHRVPHNLVASTAVSDVLVA
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                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                            Original source text: Rattus norvegicus (strain Sprague-Dawley) hypothalamus cDNA to mRNA.

Location/Qualifiers
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                                                                                                                                                                                           Enlander, M. G., Lovenberg, T. W., Baron, B. M., Lecca, L.,
Barlader, M. G., Lovenberg, T. W., Baron, B. M., Lecca, L.,
Cannon, R., Burns, J. E. and Sutcliffe, G. J. Siegel, B. W., Foye, P. E.,
Two members of a distinct subfamily of 5-hydroxytryptamine
receptors differentially expressed in rat brain Proc.
Natl. Acad. Scl. U.S. A. 90 (8), 3452-3456 (1993)
                              RATSHTSB 2240 bp mRNA linear ROD Rattus norvegicus 5-hydroxytryptamine receptor (5HTSb) m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 729.8; DB 10; Length 2240;
Pred. No. 5.5e-112;
0; Mismatches 207; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'standard name="5-hydroxytryptamine receptor"
note="putative"
                                                                                                         receptor; serotonin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               function="unknown effector coupling'
                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product="serotonin receptor"
'protein id="AAA40616.1"
'db xref="GI:310075"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="hypothalamus"
303. .1415
                                                                                                       5-hydroxytryptamine receptor;
Rattus norvegicus (Norway rat)
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'label=5-HT5b
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                                                                                                                                    Rattus norvegicus
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ACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGC
                                             595 ACGICCIGGIGGCGGCICIGGIGAIGCCACIGAGCCIGGIGAGCGAGIIGICGGCIGGG
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APPLICANT: Erlander, Mark G
APPLICANT: Erlander, Mark G
APPLICANT: Lovenberg, Timothy W
TITLE OF INVENTION: HUMAN SEROTONIN RECEPTORS, DNA ENCODING
TITLE OF INVENTION: THE RECEPTORS, AND USES THEREOF
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5968817th Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: The PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,538
FILING DATE: 19930315
CLASSIFICATION: 800
                      US-08-370-542-6
US-08-370-542-6
US-08-542-358-6
US-09-018-351-6
US-09-018-351-5
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US-09-018-351-5
US-08-117-006-5
US-08-117-006-5
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US-08-37-14
US-09-332-837-14
US-09-332-837-14
US-09-317-056-3
US-08-216-598-3
US-08-216-598-3
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US-08-216-598-3
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US-08-317-188-13
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US-09-341-446B-10
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US-08-157-185-2
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ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRE099P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08031538
Patent No. 5968817
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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STATE: CA
COUNTRY:
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-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgnZ 1/USFTO spool p/US09976782/runat 31082004 115952 10354/app query.fasta_1.1351
-D8=158ued PatentE_AA -QPMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXN=0 -UNITS=bits -GPMT=fastan -SUFFIX=h2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXN=0 -UNITS=bits -GPMT=fastan -THR MAX=100 -THR MIN=0 -ALIGN=15
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 4, 1
Sequence 4, 1
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Sequence 6
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1: /cgn2_6/ptOdata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptOdata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptOdata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptOdata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptOdata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptOdata/2/iaa/PCTUS_COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                              OM nucleic - protein search, using frame_plus_n2p model
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US-08-356-405-2
US-08-356-405-9
US-08-31-538-4
US-08-461-812-4
US-08-157-185-15
US-09-450-790A-15
US-09-332-837-15
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US-07-817-920-6
US-08-117-006-6
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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No.

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965 ATCCCCTTCTTCCTGACGGAACTCATCAGCCCACTCTGTGCCTGCAGCCTGCCCCCATC 1024
                                                                                                                                                                                                                            1085 ACAGCTTTTAACAAGAACTACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAGA 1141
                                                                                                                                                                                                                                                                                                                           272 ThralaargCysArgAlaThrValAlaPheGlnThrSerGlyAspSerTrpArgGluGln
                                                                                                                                                                          312 IleProPhePheLeuThrGluLeuValSerAlaLeuCysAlaCysSerLeuProProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Amlaiky, No. 5807691rdine
APPLICANT: Boschert, Ursula
APPLICANT: Hen, Rene
APPLICANT: Plassat, Jean-Luc
APPLICANT: Plassat, Jean-Luc
TITLE OF INVENTION: Polypeptides Having Serotonin Receptor
TITLE OF INVENTION: Activity (5HT5A), Nucleic Acids Coding for These
TITLE OF INVENTION: Polypeptides and Uses Thereof
ACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGGGAGCAG
                                                                         905 AAGGAGAGGCAGCATCATGATGGTGGAATTCTGATTGGCGTGTTTGTGCTGTGCTGG
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,405
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Matches:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR93/00650
FILING DATE: 29-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/08081
FILING DATE: 01-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: EX92004-US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: Rhone-Poulenc Rorer Inc.: 500 Arcola Road, 3C43
Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08356405 Patent No. 5807691
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Smith, Julie K
REGISTRATION NUMBER:
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STATE: PA
COUNTRY:
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US-08-356-405-2
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Mismatches:
Indels:
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                                                                                                                                                        Length:
Matches:
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                                                                                                                                                    1.24e-92
1444.50
82.85%
77.84%
67.06%
                     LENGTH: 370 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
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   SEQUENCE CHARACTERISTICS
                                                                             ; MOLECULE TYPE: protein US-08-031-538-2
                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                        Alignment Scores:
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1082 TACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAGA 1141
                                                     318 IleTrpLysSerIlePheLeuTrpLeuGlyTyrSerAsnSerPhePheAsnProLeuIle 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Amlaiky, No. 5807691rdine
APPLICANT: Boschert, Ursula
APPLICANT: Hen, Rene
APPLICANT: Hen, Rene
APPLICANT: Hen, Rene
TITLE OF INVENTION: Polypeptides Having Serotonin Receptor
TITLE OF INVENTION: Activity (5HT5A), Nucleic Acids Coding for These
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 ThrSerPheSerLeuSerThrProSerProLeuGluThrAsnHisSerLeuGlyLysAsp
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219
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92
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR93/00650
FILING DATE: 29-JUN-1992
PRIOR APPLICATION NUMBER: FR 92/08081
FILING DATE: 01-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
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                                                                                                                                                                                                                                                                                                              3: Rhone-Poulenc Rorer Inc.
500 Arcola Road, 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                           Sequence 9, Application US/08356405
Patent No. 5807691
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MEDIUM TYPE: Floppy disk
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71.31%
61.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Smith, Julie K
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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ZIP: 194
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   37
93
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   Conservative:
              Mismatches:
Indels:
Gaps:
                                                                          US-09-976-782-15 (1-1152) x US-08-356-405-2 (1-357)
71.118
60.838
47.478
Percent Similarity:
3est Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                          COUNTRY:
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WOLECULE TN
US-08-031-538-4
                                                        CITY: L
STATE:
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PheThrValArg---HisAlaThrValThrPheGlnProGluGlyAspThrCysArgGlu 277
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                 47 LeuGlyPheLeuValAlaAlaThrPheAlaTrpAsnLeuLeuValLeuAlaThrlleLeu 66
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CTAGTGCTGCTGCCTGCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCACCATCCCG
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Sutcliffe, J Gregor Erlander, Mark G Lovenberg, Timothy W

APPLICANT: APPLICANT: I

Sequence 4, Application US/08031538 Patent No. 5968817 GENERAL INFORMATION:

US-08-031-538-4

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                                                   ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5968817th Torrey Pines Road, TPC CITY: La Jolla
                                                                                                                                                                                                                                                                         COFFWARE PATENTIN STILL STORY #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,538
FILING DATE: 19930315
CLASSIFICATION: 800
ATTORNEY/AGENT INPORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: 155099P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEPHONE: 619-554-2937
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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HUMAN SEROTONIN RECEPTORS, DNA THE RECEPTORS, AND USES THEREOF
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Mismatches:
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                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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71.27%
60.85%
47.10%
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AMINO ACID
                                    73
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                                                                                                                                                                                  ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Best Local Similarity:
Query Match:
DB:
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Matches:
Conservative:
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REGISTRATION NUMBER: 28,678
REPERENCE/DOCKET NUMBER: 3651
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2122780400
TELEPHONE: 213910525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
      28,678
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448.00
48.35%
32.32%
20.80%
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TOPOLOGY: linear
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                                          740 AAGTTTCGTTTCGGC----CGCCGCCGAAGACTGTGCTGCCGTTGCCGGCCACCATGCAG 796
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         CAGCACACGCTGCGCACCCGCAGCCGCGCCTCGTTGCTCATGATCGCGCTCGCCCGGGTG 559
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                                                                                                                                                           LeuSerGluGluCysGlnValSerArgGluProSerTyrThrValPheSerThrValGly
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                                                                                                                          560 CCGTCGGCCTCATCGCCCTCGCGCCCTGCTTTGCCCGGGGCGAGGTGTGCGACGCT
                                                                                                                                                                                                                                                                                                                                                                             GCCTTCCACCTGCCGCTTGGCGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCC
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                                                                                                                                                                                                                                                     620 CGGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCCTATGCCGCCTTCTCCACCGCGGC
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APPLICANT: Branchek, Theresa
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: UNB ENCODING HUMAN 5-HTID RECEPTORS AND TITLE OF INVENTION: USES THEREOF NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1097 AAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAGA 1141
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PACEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08461812
Patent No. 5935925
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10036
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--AspalaLeuLeuGluLysLysLysLeuMetAlaAlaArgGluArg 310
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216 AlaPheTyrPheProThrLeuLeuLeuIleAlaLeuTyrGlyArgIleTyrValGluAla 235
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                                                                                                                                                                                                                                                         --GGCGCCGTCCTGCCGGGCCGA 142
                                                                                                                                                                                                                                                                                                                              143 GGGCCGCCCTTCTCTCTCTTCACGGTCCTGGTGACGCTGCTAGTGCTGCTGCTGATCGCT 202
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                                                                                                                                                                                                               10 ProProProAlaGlySerGluThrTrpValProGlnAlaAsnLeuSerSerAlaPro 29
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------TrpLysValLeuLeuValMetLeuLeuAlaLeuIleThrLeu 61
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                                                                                                                                                                                                                                                                                           30 SerGlnAsnCysSerAlaLysAspTyrIleTyrGlnAspSerIleSerLeuPro--
               390
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                 Length:
Matches:
Conservative:
                                                                                                                                               US-09-976-782-15 (1-1152) x US-08-157-185-15 (1-390)
                                                                      Mismatches:
                                                                                                                                                                                                                                                           119 AGC------
                                                                                          Indels:
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                 1.43e-23
448.00
48.35%
32.32%
20.80%
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Best Local Similarity:
 Alignment Scores:
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--------AspAlaLeuLeuGluLysLysLysLeuMetAlaAlaArgGluArg 310
                                                                                                                                                                                                                                                                                                                                                         CCGTTGCCGGCCACCATGCAGGTGAGGTCCAAGGTAAAG 814
                                                                      LeulleThrAspSerProGlySerThrSerSerValThrSerIleAsnSerArgValPro 275
                                                                                                                                                                                                                                                             ArgSerArg1leLeuLysG1nThrProAsnArgThrG1yLysArgLeuThrArgAlaG1n 255
                                                                                                                                      GAAGCACCTGATGAGGCT - - - GAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bard A. Jonathan
APPLICANT: Branchek A. Theresa
APPLICANT: Weinshank L. Richard
TITLE OF INVENTION: DNA ENCODING A HUMAN SEROTONIN
TITLE OF INVENTION: RECEPTOR (5-HT4B) AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1088 GCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTC 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41908-A-PCT-US/JPW/MAT
                                                                                                                                                                                      872 TTCCAGGTGAGCGGGACTCCTGGCGGGAGCAGAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION UNDER:
FILING DATE: 15-JUN-1995
CLASSIFICATION: 4395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/08157185 Patent No. 5985585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: White P., John
REGISTRATION NUMBER: 28.678
REFERENCE/DOCKET NUMBER: 41908
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 15:
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STRANDEDNESS: single
TOPOLOGY: linear

MOLEGULE TYPE: protein
US-08-157-185-15
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper &
                                      CTG
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914 CGAGCAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTGCTGGATCCCCTTC 973	<i>∂</i>	119 AGC
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974 TICCIGACGGAACTCATCAGCCCACTCTGTGCCTGCAGCCTGCCCCCCATCTGG 1027	8 8	143 GGGCCGCCTTCTCTGTCTTCACGGTCCTGGTGACGCTGCTAGTGCTGGTGATCGCT 202 :::
Pnellelleserbeuvalmer/YolleCysbysAspAlaCyslTpPneHlsbeuA	or or	
1028 AAAAGCATATTTCTGTGGCTTGGCTACTCCAATTCTTCTTCAACCCCCTGATTTACACA 1087	y da	203 GCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCACCATCCCGGGGTCCGTGCCTTCCAC 262
1088 GCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTC 1126 :::::::: 371 MetSerAsnGluAspPheLysGlnAlaPheHisLysLeu 383	Qy dd	263 CGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTCTCGGACGAACTAGTGGCGGCTG 322 ::
SULT 7 -08-281-526B-15 Sequence 15, Application US/08281526B	Qy Dp	323 GCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGACGTCGGCTGCTGGGCCGG 382
atent No. 6083749 GENERAL INFORMATION: APPLICANT: Bard A. Jonathan	ð 1	AGCCTGTGCCACGTGTGGATCTCCTTCGACGCCGGAGCCTGTCTGT
4 ~ H H	g & 1	
NOMBER OF SEQUENCES: 1/ CORRESPONDENCE ADDRESS: 2 STREET: 1185 Avenue of the Americas	AS AS	
ew York New York	da g	TyrSerAlaLysArgThrProLysArgAlaAlaValMetileAlaLeuValTrpValPhe
COUNTRY: U.S.A. ZIP: 10036 COMPUTER READABLE FORM:	y da	563 TCGGCGCTCTCGCGCCGCTGCTTTTGGCCGGGGGTGTGTGCGACGCTCGG 622
MEDLUM TYPE: Floppy disk COMPUTER: IEM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.24	Qy Dp	623 CTCCAGCGCGGGGGGGGGGGGGCCTCCTATGCCGCCTTCTCCACCCGGGC 679 :::
CURRENT APPLICATION DATA: APPLICATION UNBER: US/08/281,526B FILING DATE: 27-JUL-1994 CLASSIFICATION: 435	VQ.	680 GCCTTCCACCTGCCGCTGCGTGCTGTTTGTCTACCGGAAGATCTACGAGGCGGCC 739
ATTORNEY/AGENT INFORMATION: NAME: White P., John REGISTRATION NUMBER: 28,678 REFERRNCR-POCKET NIMBER: 41908-1/JPW	\trianslate{\trian	740 AAGITICGITIC
500 51	<i>&</i> €	CTGCCGTTGCCGGCCACCATGCAGGTGAGGTCCAAGGTAAAG
SEQUENCE CHARACTERISTICS: LENGTH: 390 amino acids	8	GAAGCACTGATGAGGCTGAAGTGGTGTTCACGGCACATTGCAAAGCAACGACGTGTCC
TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear	qa	::: ::: ::: ::: ::: ::: ::: : ::: :: :: :: ::: :: ::: ::: ::: ::: ::: ::: ::: :: :: :: ::: ::: ::: ::
2 E	\$ E	872 TTCCAGGTGAGCGGGGACTCCTGGCGGGAGCAGGAG
	8 & 8	CGAGCAGCCATGATGGGAATTCTGATTGGCTGTTTGTGCTGCTGCTGCTTCTTCTGCTTTTGTGCTGC
<pre>ity: 32.32\$ Mismatches: 20.80\$ Indels: 3 Gaps:</pre>	8	
US-09-976-782-15 (1-1152) x US-08-281-526B-15 (1-390)	음 :	331 PhellelleSerLeuValMetProlleCysLysAspAlaCysTrpPheHisLeuAlalle 350
59 CCCGAGACCAGCGGACCCGGGACCCCAAGCCGGAGAGGGATACTCGGTTCGACCCCG 118	ž 43	PheaspPhePheThrTrpLeudlyTyrLeuasnSerLeulleAsnProllelleThrTr

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TICCIGACGGAACTCAICAGCCCACTCIGI-----GCCTGCAGCCIGCCCCCCAICIGG 1027
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Sequence 15. Application US/09332837

Sequence 15. Application US/09332837

GENERAL INFORMATION:

APPLICANT: Bard, Jonathan

APPLICANT: Branchek, Theresa

APPLICANT: Weinstank, Richard

TITLE OF INVENTION: Methods of Obtaining Pharmaceutical Compositions

FILE REPERENCE: 41908-AAP-PCT-US

CURRENT APPLICATION NUMBER: 08/09/332,837

CURRENT FILING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.0

SEQ ID NO 15

LENGTH: 390
             TCGCCGCTCATCGCCCTCGCCCCCTCTTTGCCCCGGGCCGAGGTGTGCGACGCTCGG
                             GCCTTCCACCTGCCGCTTGGCGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCC
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APPLICANT: Bard, Jonathan A
APPLICANT: Barachek, Theresa
APPLICANT: Weinshank, Richard L
TITLE OF INVENTION: DNA ENCODING A HUMAN SEROTONIN RECEPTOR (5HT4B) AND USES THEREOF
FILE REFERENCE: 1795/4190B1A
CURRENT APPLICATION NUMBER: 08/991.1-29
PRIOR APPLICATION NUMBER: 08/281,526
PRIOR FILING DATE: 1999-11-27
PRIOR FILING DATE: 1994-07-27
PRIOR FILING DATE: 1992-11-03
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Matches:
Conservative:
Mismatches:
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                                                                  US-09-450-790A-15; Sequence 15, Application US/09450790A; Patent No. 6376243
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 390
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Pred. No.:
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Patent No. 6475746
GENERAL INFORMATION:
APPLICANT: Weinshank et al, Richard L.
TITLE OF INVENTION: Method of Obtaining A C.
TITLE OF INVENTION: Selective Compound
FILE REFERENCE: 36536-BA
CURRENT APPLICATION NUMBER: US/09/371,705
CURRENT FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Homo sapiens
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LENGTH: 390
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102 ValWetPro-----lleSerThrMetTyrThrValThrGlyArgTrpThrLeuGlyGln 119
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236 ArgSerArgIleLeuLysGlnThrProAsnArgThrGlyLysArgLeuThrArgAlaGln
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| 156 LeulleThrAspSerProGlySerThrSerSerValThrSerIleAsnSerArgValPro
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                             NAME: White, John P
RECISTRATION NUMBER: 28,678
REPERENCE/DOCKET NUMBER: 1795/39318
TELECOMMUNICATION:
TELEPHONE: 212-977-9550
                                                                                                                                                                                                                                                                                                                                                             1,56e-22
433.00
47.84%
31.55%
   ATTORNEY/AGENT INFORMATION:
NAME: White. John D
                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                          N-terminal
                                                                                        TELEPHONE: 212-977-955
TELEFAX: 212-664-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                STRANDEDNESS: unknown
                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                               linear
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CLONE: 5-HT1DB
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FRAGMENT TYPE:
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TYTSETAlaLySATHTPTOLYSATGAlaValMetIleAlaLeuValTrpValPhe
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                                               TCGGCGCTCATCGCCCTCGCGCCGCTGCTTTGGCCGGGGCGAGGTGTGCGACGTCGG
                                                                                                           CTCCAGCGCTGCCAGGTGAGCCGGGAACCC---TCCTATGCCGCCTTCTCCACCGGGGC
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/817,920
FILING DATE: 19920108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Weinshank, Richard L APPLICANT: Branchek, Theresa APPLICANT: Hartig, Paul R TITLE OF INVENTION: DNA ENCODING A TITLE OF INVENTION: USES THEREOF NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. ANDRESS:
J. ANDRESS:
COOPER & Dunham
J.REET: 30 ROCKefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 1011
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Matches:
Conservative:
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433.00
47.84%
31.55%
TELEFAX: 212-664-0525
TELEX: 422533 COOP UI
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERICS:
LENGTH: 390 amino acids
                                                                                                                                                                                         N-terminal
                                                                                  TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                          SIAMAL
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 AGC-----
                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
                                                                                                                                                                                                       IMMEDIATE SOURCE:
CLONE: 5-HT1DB
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                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                 No.:
                                                                                                                                                                                                                                                                                                                 Score:
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|331 PhelleSerLeuValMetProlleCysLysAspAlaCysTrpPheHisLeuAlalle 350
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                                                                                                                                        -----GGCCGCCGC---CGGAGAGCTGTG 772
                                                                                                                                                                         236 ArgSerArgIleLeuLysGlnThrProAsnArgThrGlyLysArgLeuThrArgAlaGln 255
                                                                                                                                                                                                           --CCGTTGCCGGCCACCATGCAGGTGAGGTCCAAGGTAAAG 814
                                                                                                                                                                                                                                           256 LeulleThrAspSerProGlySerThrSerSerValThrSerIleAsnSerArgValPro 275
                                                                                                                                                                                                                                                                               815 GAAGCACCTGATGAGGCT---GAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCC 871
                                                                                                                                                                                                                                                                                                               276 AspValProSerGluSerGlySerProvalTyrValAsnGlnValLysValArgValSer 295
                                                                                                                                                                                                                                                                                                                                                   872 TTCCAGGTGAGCGGGGACTCCTGGCGGAGCAGAAG---------GAGAGG 913
                                                                                           CTCCAGCGCTGCCAGGTGAGCCGGGAACCC---TCCTATGCCGCCTTCTCCACCCGCGGC
                         GCCTTCCACCTGCCGCTTGGCGTGGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Weinshank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HTIF RECEPTOR AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTC 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 MetSerAsnGluAspPheLysGlnAlaPheHisLysLeu 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/117,006 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect, Version:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08117006
Patent No. 5639652
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                        AAGTTTCGTTTC--
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59 CCCGAGACCAGCAGCGGACCCGGGACCCCAAGCCCGAGGGGATACTCGGTTCGACCCCG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 CGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTCTCGGACGAACTAGTGGCAGCGCTG 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    680 GCCTTCCACCTGCCGCTTGGCGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCC 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 SerileSerileSerLeuProPro---PhePheTrpArgGlnAlaLysAlaGluGluGlu 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 ThrProAlaAsnTyrLeuIleAlaSerLeuAspValThrAspLeuLeuValSerIleLeu
                                                                                                                                                                                                                                                                                                                                                                                           10 ProProAlaProAlaGlySerGluThrTrpValProGlnAlaAsnLeuSerSerAlaPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 SerGlnAsnCysSerAlaLysAspTyrIleTyrGlnAspSerIleSerLeuPro
                                                                                                                                                                                     390
124
64
149
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Mismatches:
Indels:
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                                                                                                                                                                                                         Matches:
                                                                                                                                                                                     Length:
                                                                        N-terminal
                                                                                                                                                                                                     433.00
47.84%
31.55%
20.10%
                 MOLECULE TYPE: protein HYPOTHETICAL: NO
linear
                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                       IMMEDIATE SOURCE:
CLONE: 5-HT1DB
                                                  ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                    Alignment Scores:
TOPOLOGY:
                                                                                                                             US-08-216-594-6
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                                                                                                                                                                                       No.:
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----AspAlaLeuLeuGluLysLysLysLeuMetAlaAlaArgGluArg 310
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                                                                                                                             256 LeulleThrAspSerProGlySerThrSerSerValThrSerIleAsnSerArgValPro 275
                 GGCCGCCGC - - - CGGAGAGCTGTG
                                                  236 ArgSerArgIleLeuLysGlnThrProAsnArgThrGlyLysArgLeuThrArgAlaGln
                                                                                       CTG--------CCGTTGCCGGCCACCATGCAGGTCCAAGGTAAAG
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                                                                                                                                                                                                                                        872 ITCCAGGTGAGCGGGGACTCCTGGCGGGAGCAGAAG------GAGAGG
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Parent No. 5652113
GENERAL INCRMATION:
GENERAL THORMATION:
APPLICANT: Weinshank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HTIF RECEPTOR
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1088 GCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTC 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 MetSerAsnGluAspPheLysGlnAlaPheHisLysLeu 383
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1795/39318
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                 740 AAGITICGITIC-
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TYPE: amino acid
STRANDEDNESS: unl
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US-08-216-594-6
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103 GCCACTTTCCTGTGGAACCTGGTTCCGGTCACCATCCCGCGGGTCCGTGCCTTCCAC 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323 GCGATGCCACCGAGCCTGGGGGGTGAGCTGTCGACCGGGGGGACGTCGGCTGCTGGGCCGG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 ValValCysAspPheTrpLeuSerSerAsp-----IleThrCysCysThrAlaSer 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCTTCCACCTGCCGCTTGGCGTGGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCC 739
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236 ArgSerArgIleLeuLysGlnThrProAsnArgThrGlyLysArgLeuThrArgAlaGln
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276 AspValProSerGluSerGlySerProValTyrValAsnGlnValLysValArgValSer
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                                                   Matches:
Conservative:
Mismatches:
                                                                                                                                                         US-09-976-782-15 (1-1152) x PCT-US93-00149-6 (1-390)
                                                                                                        Indels:
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LeulleThrAspSerProGlySerThrSerSerValThrSerIleAsnSerArgValPro 275
                                  GAAGCACCTGATGAGGCT---GAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCC
                                                                   AspValProSerGluSerGlySerProValTyrValAsnGlnValLysValArgValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Weinshank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Harholy, Paul R.
TITLE OF INVENTION: DNA BNCODING A HUMAN 5-HTIF RECEPTOR AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    1088 GCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTC 1126
                                                                                                                                                                                                                                                                                                                                                                                                          872 TTCCAGGTGAGCGGGGACTCCTGGCGGGAGCAGAAG-----
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00149
FILING DATE: 19930108
CLASSIPICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 1795/39318
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEPHONE: 212-664-0525
TELEX: 42253 COOP UI
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application PC/TUS9300149 GENERAL INFORMATION:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
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MEDIUM TYPE: Floppy
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; CLONE: 5-HT1DB
PCT-US93-00149-6
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Conservative: 64 Conservative: 64 State	Qy 203 GCCACTTCCTGTGGAACCTGCTGTCCACTCCCGGGGTCCGTGCTTCCAC 262	120 ValValCysAspPheTrpLeuSerSerAspIleThrCysCysThrAlaSer 13 120 ValValCysAspPheTrpLeuSerSerAspIleThrCysCysThrAlaSer 13 1443 CTGGGAACGTGGCCATGGCCTGGGCCGACGGGCCATCACAGGCACCTGCAG 50 137 IleLeuHisLeuCysValIleAlaLeuAspArgTyrTrpAlaIleThrAspAlaValGlu 15 503 CACAGGCTGCGCAGCCGGGCCTGTTGCTCATGATGGGCTGGCCGGGTGCG 56 157 TyrSerAlaLysArgThrProLysArgAlaAlaValMetIleAlaLeuValTrpValPhe 17 177 CATLESER 11 68-71 16	623 CTCCAGGGCTGCAGGTGAGACCCTOCTATGCGCCTTCTCCACCCGGGG 6.::	Oy 773 CTG
Db 296AspalaLeuLeuGluLysLysLysLeuMetalaAlaArgGluArg 310 Qy 914 CGAGCAGCATGATGGGAATTCTGATTGGCTGTTTGTGCTGGATCCCTTC 973 ::: ::: ::::	RESULT 15 US-08-370-542-6 is Sequence 6, Application US/08370542 is Sequence 6, Application US/08370542 is GENERAL INFORMATION: APPLICANT: Meinshark, Richard L. APPLICANT: Branchek, Theresa is APPLICANT: Hartig, Paul R. ITILE OF INVENTION: USES THEREOF NUMBER OF SEQUENCES: 12 CORRESPONDENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSES: Cooper & Dunham STREET: 30 Rockefeller Plaza	A "CATANATION	US/00 US/00 ION: 28,0 ER: MATIC	JUNFORMATION FOR SEQ ID NO.: 6: SEQUENCE CHARACTERISTICS: LENGTH: 398 amino acids TYPE: amino acid TOPOLOGY: unknown MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO SAMI-SENSE: No SAMI-SENSE: No ALIGHMENT TYPE: No SAMI-SENSE: NO SAMI-S

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311 LysAlaThrLysThrLeuGlyIleIleLeuGlyAlaPheIleValCysTrpLeuProPhe 330
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CCTGCCCCCATCTGG 1027		pPheHisLeuAlaIle 350
974 ITCCTGACGGAACTCATCAGCCCACTCTGTGCCTGCAGCCTGCCCCCCATCTGG 1027		331 PhellelleSerLeuValMetProlleCysLysAspAlaCysTrpPheHisLeuAlalle 350
TTCCTGACGGAACTCATCAGCC	:::::::::::::::::::::::::::::::::::::::	PhellelleSerLeuValMetP
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homo sapien pan troglod fugu rubrip

bombyx mori

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Perfect score:

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Sequence:

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P30940 rattus norv
O42385 fugu rubrip
P32304 mus musculu
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01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
5-hydroxytryptamine 5B receptor (5-HT-5B) (Serotonin receptor) (MR22).
HTRSB OR SHT5B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=33234515; PubMed=7682702; Erlander M.G., Lovenberg T.W., Baron B.M., de Lecea L., Danielson P.E., Racke M., Slone A.L., Siegel B.W., Poye P.E., Cannon K., Burns J.E., Sutcliffe G.J.; Siegel B.W., Poye P.E., Cannon K., Burns J.E., Sutcliffe G.J.; Fydroxytryptamine receptors differentially expressed in rat brain."; proc. Natl. Acad. Sci. U.S.A. 90:3452-3456(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIGURE 333:25-31(1993).

FUNCTION: This is one of the several different receptors for 5-bydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins. Probably involved in arxiety and depression.

SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: Brain; in the CAl region of hippocampus, the medial abbenula, and raphe nuclei.

SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

STRONGEST TO THE OTHER SHT-5 SUBTYPE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=94039744; PubMed=8224165;
Misden W., Parker E.M., Mahle C.D., Grisel D.A., Nowak H.P.,
Vocca F.D., Felder C.C., Seeburg P.H., Voigt M.M.;
"Cloning and characterization of the rat 5-HTSB receptor. Evidence that the 5-HTSB receptor couples to a G protein in mammalian cell
                                                                                P34969
Q25414
P28565
P49145
P50407
O08890
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P28566
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P35404
Q9n2d9
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Q9n298
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Q25322
                             P79748
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                                                                                                                SHID_RABIT
SH7_CAVPO
SH1F_CAVPO
SH1F_HUWAN
SH1B_DIDMA
SH1F_PANTR
SH1F_MOUSE
GREZ_BALAM
SH1E_PANTR
SH1E_PANTR
                                                                                                                                                                                                                        5H7 RAT
OAR1 LOCMI
OAR2 LOCMI
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SH1A_FUGRU
                                                              MOUSE
                                         SH1A MOUSE
                                                  SHIA RAT
SHID MOUSE
SHT HELVI
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SH1D RAT
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STRAIN-Sprague-Dawley; TISSUE-Brain;
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NCBI_TaxID=10116;
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pan troglod
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P20905 drosophila
P11614 canis famil
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                       Compugen Ltd.
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Copyright (c) 1993 - 2004 Compuq
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Jatabase :

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Result

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                                                        LeucyscysthralaserileTrpAsnValAlaAlaIleAlaLeuAspArgTyrTrpThr
                                                                                                             |||:::
| AlaileThrTrpAlaLeuSerAlaLeuIleAlaLeuAlaProLeuLeuPheGlyTrpGly
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                             CTGTGCTCCCCCCCCCCTCGGGAACGTGGCGGCCATCGCCCTGGGCCGCGACGGGGCC
                                                                                          ATCACACGGCACCTGCAGCACGCTGCGCACCCGCAGCCGCGCCTCGTTGCTCATGATC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MatDLINE=93196607; PubMed=8450829;
Matthes H., Boschert U., Amiliky N., Grailhe R., Plassat J.-L.,
Muscatelli F., Mattei M.-G., Hen R.;
Muscatelli F., Mattei M.-G., Hen R.;
deves F. hydroxytryptamine5A and 5-hydroxytryptamine5B receptors
define a new family of serotonin receptors: cloning, functional
expression, and chronosomal localization.";
Mol. Pharmacol. 43:313-319(1993).
119 ArgTrpGlnLeuGlyArgSerLeuCysHisValTrpIleSerPheAspVal---
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01-JUL-1993 (Rel. 26, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
5-hydroxytryptamine 5B receptor (5-HT-5B) (Serotonin receptor)
HTRSB OR SHTSB.
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(GLCNAC. ) (POTENTIAL).
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                           anxiety and depression.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Expressed predominantly in the central nervous system; in the hippocampus, habenula, and the doral raphe.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
STRONGEST TO THE OTHER 5HT-5 SUBTYPE RECEPTORS.
FUNCTION: This is one of the several different receptors for 5-hydroxtryptamine (serotonin), a biogenia-hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins. Probably involved in
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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MGD; MGI:96284; Htr5b.

InterPro; 1FP000276; GPCR_Rhodpsn.

Pronoil, 7tm 1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP_F1 1; 1.

PROSITE; PS050262; G_PROTEIN_RECEP_F2 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family.
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S. TRACELLULAR (POTENTIAL).

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               79 ArgvalargAlaPheHisArgValProHisAsnLeuValAlaSerThrAlaValSerAsp 98
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
5-hydroxytryptamine 5A receptor (5-HT-5A) (Serotonin receptor)
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 Mismatches:
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                Indels:
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                                  Gaps:
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                49.37$
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
Puhl H.L. III, Ikeda Guthrie con an anitor (aww.cdna.org).";
Submitted (ARR-2002) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: This is one of the several different receptors for 5-
- FUNCTION: This is one of the biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins.
-! SUBCELUMAR LOCATION: Integral membrane protein.
-! SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
SIRONGEST TO THE OTHER SHT-5 SUBTYPE RECEPTORS.
                                                           MEDLINE=95080386; PubMed=7988681; Rees S., den Daas I., Foord S., Goodson S., Bull D., Kilpatrick G., Lee M.; "Cloning and characterisation of the human 5-HT5A serotonin
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N-LINKED (GLCNAC. . .) (POTENTIAL)
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS50262; GPROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family.
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EXTRACELLULAR (POTENTIAL).
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EMBL; X81412; CAA57168.1; JOINED.
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PIR; I37107; I37107.
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664

242

841

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Percent Similarity:

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6
21
120
357 AA;
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Best Local Similarity:
  182
199
220
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342
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Matthes H., Boschert U., Amlainy N., Grailhe R., Plassat J.-L.,
Muscatelli F., Mattei M.-G., Hen R.,
"Mouse 5-hydroxytryptamine5A and 5-hydroxytryptamine5B receptors
of define a new family of serotonin receptors: cloning, functional
expression, and chromosomal localization.";
Mol. Pharmacol. 43:313-319(1993).

I. FUNCTION: This is one of the several different receptors for 5-
hydroxytryptamine (serotonin), a biogenic hormone that functions
as a neurotransmitter, a hormone, and a mitogen. The activity of
this receptor is mediated by G protein.

I. SUBCELLUIAR LOCATION: Integral membrane protein.

I. SUBCELLUIAR LOCATION: Integral membrane protein.

I. TISSUE SPECIFICITY: Expressed predominantly in the central nervous
system; in the cerebral cortex, hippocampus, habenula, olfactory
bulb and granular layer of the cerebellum.

I. SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

STRONGEST TO THE OTHER SHT-5 SUBTYPE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                         TACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAG 1138
                                                MEDINE-93099851; PubMed-1464308;
Plassat J.-L., Boschert U., Amlaiky N., Hen R.;
"The mouse 5HT5 receptor reveals a remarkable heterogeneity within
                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
5-hydroxytryptamine 5A receptor (5-HT-5A) (Serotomin receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0237; GPCRRHODOPSN.
PROSITE; PS00237; GPCRHODOPSN.
PROSITE; PS50262; G-PROTEIN RECEP_F1_1; 1.
PROSITE; PS50262; G-PROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family.

BOMAIN

EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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InterPro; IPR000276; GPCR_Rhodpsn.
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MEDLINE=93196607; PubMed=8450829;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5HT1D receptor family.";
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                                                                                                                                                           STANDARD;
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SEQUENCE FROM N.A.
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|183 GluThrTyrSerGluProSerGluGluCysGlnValSerArgGluProSerTyrThrVal
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N-LINKED (GLCNAC. .) (POTENTIAL)
BY SIMILARITY.
                                                  6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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                           S (FOLENITAL);
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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Matches:
Conservative:
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FT DOMAIN 64 78 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 79 99 2 (POTENTIAL). FT DOMAIN 100 115 EXTRACELLULAR (POTENTIAL). FT DOMAIN 138 158 (CYTOPLASMIC (POTENTIAL). FT DOMAIN 138 159 181 4 (POTENTIAL). FT DOMAIN 220 282 CYTOPLASMIC (POTENTIAL). FT TRANSMEM 199 5 (POTENTIAL). FT TRANSMEM 321 34 5 (POTENTIAL). FT TRANSMEM 321 341 7 (POTENTIAL). FT CARBOHYD 6 6 (POTENTIAL). FT CARBOHYD 21 21 N-LINKED (GLONAC) (POTENTIAL). FT CARBOHYD 6 6 6 N-LINKED (GLONAC) (POTENTIAL). FT CARBOHYD 21 21 N-LINKED (GLONAC) (POTENTIAL). FT CARBOHYD 6 6 6 N-LINKED (GLONAC) (POTENTIAL). FT CARBOHYD 7 192 BY SIMILARITY. SQ SEQUENCE 357 AA, 40672 MM, 8C498A50C88408BS CRC64; FT CARBOHYD 6 6 884 SCC684108BS CRC64; FT DISTURTIAL 120 192 BY SIMILARITY. SQ SEQUENCE 357 AA, 40672 MM, 8C498A50C88408BS CRC64; FT CARBOHYD 6 6 884 Mismatches: 81 SCC64; FT CARBOHYD 6 6 885 Mismatches: 81 Gaps: 71.27\$ DOWERY MATCh: 71.27\$ DOWERY MATCh: 71.00\$ DOWE	110 TCGACCCGAGGGGCCGTCTGCCGGGCCGGCGCGGCGCGG
SUI SA_	DT 0-UTN-1994 (Rel. 29, Created) DT 0-UTN-1994 (Rel. 29, Last sequence update) DT 0-UTN-1995 (Rel. 32, Last amnotation update) DT 0-NOV-1995 (Rel. 32, Last amnotation update) DE 5-MACROWYLYPTHAMINE 5A receptor (5-HT-5A) (Serotomin receptor) DE 6-MACROWYLYPTHAMINE 5A receptor (5-HT-5A) (Serotomin receptor) STREALIN STREAMS (Rel. 32, Last amnotation update) OC MARMENIA: Eutheria; Rodentia; Sciurognathi, Muridae, Murinae; Rattus. NUEL TaxID-10116; RE 5ENDARGE FROW N.A. RE 6ENDARGE FROW N.A. RE 7 THE

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[6]
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262
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                                                                  GTGAGGTCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGTGGTGTTCACGGCACATTGC 856
                                                                                                                                                          857 AAAGCAACGGIGICCTICCAGGIGAGCGGGGACTCCTGGCGGGAGCAGAAGGAGAGGCGA
                                                                                                            MEDLINE=92246962; PubMed=1315531; Hamblin M.W., Metcalf M.A., McGuffin R.W., Karpells S.; Hamblin M.W., Metcalf M.A., McGuffin R.W., Karpells S.; "Molecular cloning and functional characterization of a human 5-HT1B serotonin receptor: a homologue of the rat 5-HT1B receptor with 5-HT1D-like pharmacological specificity."; Biochem. Biophys. Res. Commun. 184:752-759(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92302275; PubMed=1351684; Demchyshyn L., Sunahara R.K., Miller K., Teitler M., Hoffman B.J., Kennedy J.L., Seeman P., van Tol H.H.M., Niznik H.B.; "A human serotonin 1D receptor variant (SHTID beta) encoded by an intronless gene on chromosome 6."; Proc. Natl. Acad. Sci. U.S.A. 89:5522-5526(1992).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Human sercionin ID receptor is encoded by a subfamily of two
"distinct genes: 5-HTID alpha and 5-HTID beta.";
Proc. Natl. Acad. Sci. U.S.A. 89:3630-3634(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 ArgSerTyrSerSerAlaPheLysValPhePheSerLysGlnGln 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-WAR-2004 (Rel. 43, Last amotation update)
5-WARACXYUTYPEAmine 1B receptor (5-HT-1B) (Seroto: (5-HT-1D-beta) (Serotoin 1D beta receptor) (S12)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A.
MEDLINE=92218412; PubMed=1559993;
Leryy F.O., Gddermann T., Perez-Reyes E., Birnbaumer M., Kaumann A.J.,
Birnbaumer L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Human serotonin1B receptor expression in Sf9 cells: phosphorylation, palmitoylation, and adenylyl cyclase inhibition."; Biochemistry 32:11727-11733(1993).
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SUBCELLULAR LOCATION: Integral membrane protein.
PTM: Phosphorylated, and palmitoylated. Desensitization of the receptor may be mediated by its phosphorylation.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Strongest to the other 5HT-1 subtype receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92210526; PubMed=1348246;
Jin H., Oksenberg D., Ashkenazi A., Peroutka S.J., Duncan A.M.V.,
Rozmahel R., Yang Y., Mengod G., Palactios J.M., O'Dowd B.F.;
"Characterization of the human 5-hydroxytryptaminelB receptor.";
J. Biol. Chem. 267:5735-5738(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                           "Molecular cloning of a human serotonin receptor (512) with a pharmacological profile resembling that of the 5-HTID subtype."; J. Biol. Chem. 267:7553-7562(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kopatz S.A., Aronstam R.S., Sharma S.V.; "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie CDNA resource center (www.cdna.org)."; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Veldman S.A., Bienkowski M.J.;
"Clonting and plarmacological characterization of a novel human hydroxytryptaminelD receptor subtype.";
Mol. Pharmacol. 42:439-444(1992).
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Ng G.Y.K., George S.R., Zastawny R.L., Caron M., Bouvier M.,
Dennis M., O'Dowd B.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (APR-2000) to the EMBL/GenBank/DDBJ databases
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Biochem. Biophys. Res. Commun. 205:1194-1200(1994).
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"Silver project.";
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974 TICCTGACGGAACTCATCAGCCCACTCTGT-----GCCTGCAGCCTGCCCCCCCATCTGG 1027
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| 102 ValMetPro-----IleSerThrMetTyrThrValThrGlyArgTrpThrLeuGlyGln 119
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                                                                ::: ||||||| | ||||||| ThrProAlaAsnTyrLeuIleAlaSerLeuAlaValThrAspLeuLeuValSerIleLeu 101
                                                                                                         GCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGACGTCGGCTGCTGGGCCGG 382
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ValSerGluCysValValAsnThrAspHisIleLeuTyrThrValTyrSerThrValGly
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1D 5HIB PANTR STANDARD; PRT; 390 AA,
AC P60020;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
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GO; GO:0001887; P:serotonin receptor activity; TAS.
GO; GO:0001887; P:esrotonin receptor activity; TAS.
GO; GO:0007187; P:e-procein signaling, coupled to cyclic nucl. . .; TAS.
GO; GO:000786; P:synaptic transmission; TAS.
InterPro; IPR00027; GPCR_Rhodpsn.
PROSITE; PR00237; GPCRHODPSN.
PROSITE; PS00237; GPRCHENDENEN.
PROSITE; PS00237; GPROTEIN RECEP F1.; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Multigene femily; Lipoprotein; Palmitate; Phosphorylation;
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F -> C in dbSNP:130060).
FTId=VAR 011715.
F -> L (in dbSNP:130061).
/FTId=VAR 011831.
/FTId=VAR 011831.
/FTId=VAR 011832.
E -> K (in dbSNP:130064).
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CYTOPLARMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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EMBL; AY22527; AA067712.1; -.
EMBL; AL049995; CAB51837.1; -.
PIR; UNO268; UN0268.
Genew; HGNC: 5287; HTR1B.
MIM; 182131; -.
   ANNOTATED
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ArgSerArgIleLeuLysGlnThrProAsnArgThrGlyLysArgLeuThrArgAlaGln 255
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LysAlaThrLysThrLeuGlyIleIleLeuGlyAlaPheIleValCysTrpLeuProPhe 330
                                        GGGCCGCCCTTCTCTGTCTTCACGGTCCTGGTGGTGACGCTGCTAGTGCTGCTGATCGCT 202
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  SerGlnAsnCysSerAlaLysAspTyr1leTyrGlnAspSer1leSerLeuPro----
                                                                                -- TrpLysValLeuLeuValMetLeuLeuAlaLeuIleThrLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute of There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/ r send an email to license@ibs.sib.ch).
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MINTE OF CHAR-2000) to the EMBL/GenBank/DDBJ databases.

MINTERON: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that inhibit adenylate cyclase activity (By similarity).

MINTERIAR LOCATION: Integral membrane protein.

PIN: Phosphorylated, and palmitcylated. Desensitization of the receptor may be mediated by its phosphorylation (By similarity). SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

Strongest to the other 5HT-1 subtype receptors.
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EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
15-MAR-2004 (Rel. 43, Last annotation update)
5-hydroxytryptamine 1B receptor (5-HT-1B) (Serotonin receptor)
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CD874DC7EB44CF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB041371; BAA94456.1; -. PROSITE; PS00237; G PROTEIN RECEP_F1_1; 1. PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1. G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate; Phosphorylation. DOMAIN
                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eute.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan
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                                                                                                                                                                                         Kitano T., Kobayakawa H., Saitou N.;
"Silver project.";
Submitted (APR-2000) to the EMBL/GenB
                                                            Pan troglodytes (Chimpanzee).
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                                                                                                                               24 AsnLeuSerHisAsnCysSerAlaAspSerTyrIleTyrGlnAspSerIleAlaLeuPro 43
                                                                                                                                                                                                                                                                56 ThrLeuAlaThrThrLeuSerAsnAlaPheValIleAlaThrValTyrArgThrArgLys 75
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|114 GlyGlnValValCysAspPheTrpLeuSerSerAsp-
US-09-976-782-15 (1-1152) x 5H1B_SPAEH (1-386)
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                                                                                                                                                                                                                                                                                                                                hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that inhibit adenylate
                                                                                                                                                                                                                                                                                                                                                                                            SUBSTITUTE LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Strongest to the other 5HT-1 subtype receptors.
                                                                                                                                                                                                                                                                                Devor E.J., Nevo E.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This is one of the several different receptors for
                                                                                                                                                                  Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Spalacinae,
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
BY SIMILARITY.
S-palmitoyl cysteine (Potential).
7A006E021A44B7F4 CRC64;
                                                                                    10-0CT-2003 (Rel. 36, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
5-hydroxytryptamine 1B receptor (5-HT-1B) (Serotonin receptor).
HTR1B OR 5HT1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR00015; GPCR_Rhodpsn.
Pfam; PF00001; TR000137; GPCR_Rhodpsn.
PRINTS; PR00237; GPCRHHODDPSN.
PROSITE; PS00237; G_PROTBIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTBIN_RECEP_F1_2; 1.
GPOTCTEIN coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.
DOMAIN
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CYTOPLASMIC (POTENTIAL).
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Indels:
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Best Local Similarity:
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             345 AlailePheAspPhePheAsnTrpLeuGlyTyrLeuAsnSerLeuIleAsnProileile 364
                                                                                                                                                                                                                                                                                                                           Sgombick J.M., Bard J.A., Kucharewicz S.A., Urguhart D.A.,
Weinshank R.L., Branchek T.A.;
"Molecular cloning and pharmacological characterization of guinea pigg
"Molecular ceoptors.";
Neuropharmacology 36:513-524(1997).
-!- FUNCTION: This is one of the several different receptors for 5-
hydroxytryptamine (seronin), a biogenic hormone that functions
as a neurotransmitter, a hormone, and a mitogen. The activity of
this receptor is mediated by G proteins that inhibit adenylate
                                                                                                                                                                                                                                                                                                                                                                                                                                       cyclase activity.
SUBCELIOLAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Strongest to the other 5HT-1 subtype receptors.
                                                                                                                                                                                                                              Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                         15-UUL-1998 (Rel. 36, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
5-hydroxytryptamine lB receptor (5-HT-1B) (Serotonin receptor)
                                                                            365 TyrThrMetProAsnGluAspPheLysGlnAlaPheHisLysLeu 379
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InterPro; IPR000276; GPCR_Rhodpsn.
PRIMTS; PR000237; FRIMI: 1.
PRINTS; PR001237; GPCRHHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Lipoprotein; Palmitate.
DOMAIN
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGTTCACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGG 898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---CCGTTG 781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 SerSerValThrSerIleAsnSerArgAlaProGluValProCysAspSerGlySerPro 283
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70 IleAlaThrValTyrArgThrArgLysLeuHisThrProAlaAsnTyrLeuIleAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACGCCGGAGCCTGTCTTGTGCTGCCCCCGCCGCCTCGGGAACGTGGCGGCCATCGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 AspargTyrTrpalaileThrAspAlaValGlyTyrSerAlaLysArgThrProArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            590 CTCTTTGGCCGGGGCGAGGTGTGCGACGCTCGGCTCCAGCGCTGCCAGGTGAGCCGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGGCCACCATGCAGGTGCAAGGTAAAGGAAGCACCT---GATGAGGCTGAAGTG
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                                                      S-palmitoyl cysteine (Potential)
CO57CABOA7FEE3C6 CRC64;
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125
61
159
12
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                                                                                                                                                                                                                          Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------GGCCGCCGC---CGGAGAGCTGTGCTG-
                                                                                                                                                                   Length:
Matches:
                               BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCCTGGTGGTGACGCTGCTAGTGCTGATCGCTGCCACTTTCCTGTGGAACCTGCTG 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValLeuLeuValLeuLeuLeuAlaLeuPheThrLeuAlaThrThrLeuSerAsnAlaPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCWAC. . .) (POTENTIAL)
N-LINKED (GLCWAC. . .) (POTENTIAL)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-palmitoyl cysteine (Potential).

G - S (IN RBF. 1 AND 3).

Q -> R (IN RBF. 1 AND 3).

MISSING (IN RBF. 1 AND 3).
                                                                                               6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                          4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                         2 (FOTENTIAL) .
EXTRACELLULAR (POTENTIAL)
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C22EBC077C6C897D CRC64;
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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                                                                                     941 ATTGGCGTGTTTGTGCTGTGCTGGATCCCCTTCTTCCTGACGGAACTCATCAGCCCACTC 1000
                                                                                                                                             -----GCCTGCAGCCTGCCCCCCATCTGGAAAGCATATTTCTGTGGCTTGGCTAC 1054
                                                                                                                                                                                                   1055 TCCAATTCTTCTTCAACCCCCTGATTTACACAGCTTTTAACAAGAACTACAACAATGCC 1114
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                                                -GAGAGGGAGCAGCCATGATGGTGGGAATTCTG 940
                                                                                                     339 CysLysAspAlaCysTrpPheHisMetAlaIlePheAspPhePheThrTrpLeuGlyTyr 358
    ---AspAlaLeuLeu 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=New Zealand white; TISSUE=Saphenous vein;
Wurch T., Cathala C., Palmer C., Valentin J.P., John G.,
Colpaert F.C., Pauwels P.J.;
"Molecular cloning and identification of a rabbit saphenous vein 5-HT
IDB receptor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Naunyn Schmiedebergs Arch. Pharmacol. 354:237-244(1996).

-!- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that inhibit adenylate cyclase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harwood G.S., Lockyer M., Giles H., Fairweather N.; "Cloning and characterisation of the rabbit 5-HIID alpha and 5-HIID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to family 1 of G-protein coupled receptors. Strongest to the other 5HT-1 subtype receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=New Zealand white;
STRAIN=New Zealand white;
MEDLINE=97032156. PubMed=8878052;
Bard J.A., Kucharewicz S.A., Zgombick J.M., Weinshank R.L.,
Branchek T.A., Cohen M.L.;
"Differences in ligand binding profiles between cloned rabbit and
human 5-HTID alpha and 5-HTID beta receptors: ketanserin and
methlothepin distinguish rabbit 5-HTID receptor subtypes:";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
5-hydroxytryptamine 1B receptor (5-HT-1B) (Serotonin receptor)
                                                                                                                                                                                                                                                                                                                                           390 AA
 284 ValTyrValAsnGlnValLysValArgValSer-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurosci. Res. Commun. 18:155-162(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96130324; PubMed=8543023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                beta receptors.";
FEBS Lett. 377:73-76(1995).
                                                                                                                                                                                                                                                        1115 TTCAAGAGCCTC 1126
                                                                                                                                                                                                                                                                                  379 PheHisLysLeu 382
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                              GAGCAGAAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            (5-HT-1D-beta).
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Proc. Natl. Acad. Sci. U.S.A. 87:8940-8944 (1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1052 TACTCCAATTCTTTCTTCAACCCCCTGATTTACACAGCTTTTAACAAGAACTACAACAAT 1111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuGluLysLysLysLeuMetAlaAlaArgGluArgLysAlaThrLysThrLeuGlyIle 318
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                                                                                         286
                                                                                                                                                                                                                                                                                           751
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ---CCG 778
                                                                                                                                                                               CTGCTCTTTTGGCCGGGGCGAGGTGTGCGACGCTCGGCTCCAGGCGCTGCCAGGTGAGCCGG 646
                                                                                                                                                                                                                        ---PhePheTrpArgGlnAlaLysAlaGluGluGluValSerGluCysLeuValAsnThr 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 ProAsnArgThrGlyLysArgLeuThrArgAlaGlnLeuIleThrAspSerProGlySer 263
  CTGGGCCGCGACGGGCCATCACACGGCACCTGCAGCACACACGCTGCGCACCCCGCAGCCGC
                                           LeuaspargTyrTrpalaileThraspalavalGluTyrSerAlaLysArgThrProLys 164
                                                                                                                                   165 ArgAlaAlaIleMetIleArgLeuValTrpValPheSerIleCysIleSerLeuProPro 184
                                                                                                                                                                                                                                                                    647 GAA----CCCTCCTATGCCGCCTTCTCCACCCGCGGCGCCCTTCCACCTGCCGCTTGGCGTG
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                                                                                            GCCTCGTTGCTCATGATCGCGCTCGCCCGGGTGCCGTCGGCGCTCATCGCCCTCGCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ol-rbb-1991 (Rel. 17, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
5-hydroxytryptamine receptor 1 (5-HT receptor) (Serotonin receptor)
5-HTTOR SHT-R1 OR CG12073.
                                                                                                                                                                                                                                                                                                                                                           GTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCCAAGTTTCGTTTC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neoptera; Endopterygota; nexapoda; Insecta; Pterygo
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -------GGCCGCCGC---CGGAGAGCTGTGCTG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 ProvalTyrValAsnGlnValLysValArgValSer-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           564 AA
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last seq
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Addans M.D. Celniker S.E., Holt K.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Adams M.D. Celniker S.E., Holt K.A., Evans C.A., Gocayne J.D.,
Adams M.D. Celniker S.E., Holt K.A., Evans G.A., Galle R.F.,
Adams G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Ffeiffer B.D.,
Abril J.F., Agbayani A., An H.J., Andrews-Frankoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.J., Andrews-Frankoch C., Baldwin D.,
Abril J.F., Bench P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Broketein P., Brottier P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Borkova D., Botchan M.R., Bouck J., Broketein P., Brottier P.,
A Bottler K., Gabriellan A.B., Galle S., Mays A.D., Davies P.,
A Bottler K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Burtis K.C., Brawn D.R., Garlell J.H., Galles E., Houck J.,
Adali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Lasko G. Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Alalai M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,
Liu X., Mattel B., McIntoen T.C., Miratt C., Miratt S., Moshrefi A.,
Alalai M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,
Liu X., Mattel B., McIntoen T.C., Miratt C., Miratt S., Mollen D.,
Alalai M., Kalush P., Miron K., Murphy B., Murphy L., Mirany D.M., Nelson D.L.,
Alaracolo M., Pittenan G.S., Pan S., Pollard J., Wang X.,
Alala M., Woodage T., Simpson M., Strong R., Sun E.,
Shie E., Spradling A.C., Stapleton M., Strong R., Wang X.,
Williams S.M., Woodage T., Simpson M., Strong R., Williams S.M., Woodage T., Simpson M., Zhong K., Zhan M., Zhong K., Williams S.M., Woodage T., Simpson M., Strong R., Simb H.,
Williams S.M., Woodage T., Shore K., Will S., Shan M., Strong R.,
C., Siden-Kiamog I., 
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-!- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins which activate adenylate
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TISSUE SPECIFICITY: Head.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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PROSITE; PS00237; G-PROTEIN RECEP_F1 1; 1.
PROSITE; PS50262; G-PROTEIN RECEP_F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Repeat. 29 51 0 (POTENITAL).
TRANSMEM 165 188 1 (POTENITAL).
STRAIN=Berkeley;
MEDLINE=20196006; Pubmed=10731132;
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InterPro, IPR000276; GPCR Rhodpsn.
InterPro, IPR007455; Serglycin.
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Pfam; PF04360; Serglycin; 1.
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248 AlaserileLeuAnnLeuCysAlaileSerValAspArgTyrLeuAlaileThrLysPro 497 CTGCAGCACACGCAGCCCGCAGCCGCGCTTGCTCATGATCGCCCCGG 268 LeuGluyrGlyvalLysArgThrProArgArgMetMetLeuCysValGlyIleValTrp 557 GTGCCGTCGGCGCTCATCGCCCTCGCGCGCGCGGGCGGGC	361 ThrHisLeuGlndlnAlaLeuAsndlyThrGlySerProSerAlaProGlnAlaProPro 779 TTGCCGGCCACCATGCAGGTGAGGTAAAGGA	Qy 941 ATTGGCGTGTGTGGGATCCCTTCTTCTGGAACTCATAGCCCACTC 1000 bb 460 MetSeralaPheThrValCysTrpLeuProPhePheIleLeuAlaLeuIleArgProPhe 479 Qy 1001 TGTGCCTGCGCCCCCATCTGGAAAGCATATTCTGTGGCTACTCCAAT 1060 bb 480 GluThrMetHisValProAlaSerLeuSerSerLeuPheLeuTrpLeuGlyTyrAlaAsn 499 Qy 1061 TCTTCTTCAACCCCCTGATTTACACAGCTTTTAACAAGAACTACAACAATGCTTCAAG 1120 Bb 500 SerLeuLeuAsnProIleIleTyrAlaThrLeuAsnArgAspPheArgLysProPhedIn 519 Qy 1121 AGCCTC 1126 1121 AGCCTC 1126 520 GluIle 520 GluIle	RESULT 12 5H1D_CANFA 1D = 5H1D
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                                                                                                                                                                                                                          MEDLINE=92062181; PubMed=1659418;
Maenhaut C., van Sande J., Massart C., Dinsart C., Libert F.,
Monferini E., Giraldo E., Ladinsky H., Vassart G., Dumont J.E.;
"The orphan receptor cDNA RDC4 encodes a 5-HTID serotonin receptor.";
Biochem. Biophys. Res. Commun. 180:1460-1468(1991).
                                                                                                                                                                                                                                                                                                                                                  "Expression and pharmacological characterization of a canine 5-hydroxytryptaminelD receptor subtype.";
Mol. Pharmacol. 40:1036-1042(1991)
-!- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that inhibit adenylate
                                                                                                                                                                                                                                                                                                                                                                                                                                             cyclase activity.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Strongest to the other 5HT-1 subtype receptors.
                                                              O
                                    Libert F., Parmentier M., Lefort A., Dinsart C., van Sande J., Maenhaut C., Sinons M.-J., Dumont J.E., Vassart G.; "Salective amplification and cloning of four new members of the protein-coupled receptor family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                       MEDLINE=90245610; PubMed=2159630;
Libert F., Parmentier M., Lefort A., Dumont J.E., Vassart G.;
"Complete nucleotide sequence of a putative G protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                 MEDLINE=92100052; PubMed=1758439;
Zgombick J.M., Weinshank R.L., Macchi M., Schechter L.E.
Branchek T.A., Hartig P.R.;
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                            Dinsart C., var
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PROSITE, PROOZJ7; GPCRRHODOPSN.
PROSITE; PSO0237; G PROTEIN RECEP F1 1; 1.
PROSITE; PSO262; G_PROTEIN_RECEP_F1_2; 1.
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InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                        MEDLINE=89242119; PubMed=2541503;
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Multigene family.
DOMAIN 1
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                                                                                                                                                                                                                                                                                                                              GAGGCCGCTAGCCTTTCAGTGGCCACCGCCGCGTTGCCCTTGCCCTGGGACCCGAGACC
                                                                                                                                                                                                                                                                                                                                                    188 GIGCIGCIGAICGCIGCCACIIICCIGIGGAACCIGCIGGIICCGGICACCAICCCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 SerileileThrMetAlaThrAlaLeuSerAsnAlaPheValLeuThrThrilePheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 GICCGIGCCTICCACCGCGIGCCGCAIAACTIGGIGGCCTCGACGGCCGICTCGGACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 ThrarglysLeuHisThrProAlaAsnTyrLeuIleGlySerLeuAlaMetThrAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 LeuvalSerIleLeuvalMetProIleSerIleAla-----TyrThrThrArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CysCysThrAlaSerIleLeuHisLeuCysValIleAlaLeuAspArgTyrTrpAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          488 ACACGGCACCTGCAGCACACGCTGCGCACCGCGCGCGCCCTCGTTGCTCATGATCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               548 CTCGCCCGGGTGCCGTCGGCGCTCATCGCCCTCGCCGCCGCTGCTCTTTGGCCGGGGCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       665 TICTCCACCCGCGGCGCCTTCCACCTGCCGCTTGGCGTGGTGCCGTTTGTCTACCGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 ThrThrAlaGlnLeuIleThrGlySerAlaGlySerSerLeuCysSerLeuSerProSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTAGTGGCAGCGCTGGCCATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGACGT
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. .) (POTENTIAL) . .) (POTENTIAL)
                                                                 8E6406DCE2123EE4 CRC64;
                                                                                                                                  377
121
66
142
68
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Mismatches:
    N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                               SIMILARITY
                                                                                                                                                        Matches:
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                      N-LINKED (BY SIMILAR
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                                                                   41882 MW;
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                                                                                                                                    78e-16
                                                                                                                                                   441.00
47.10%
30.48%
                                                                                                                                                                                                                    20.47%
    17
21
111
377 AA;
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                                                                                                                Alignment Scores:
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CYTOPLASMIC (POTENTIAL)
                                                                                                                                                           MW.
                                                                                                                                                                                             1.1e-15
440.00
51.01%
34.78%
20.43%
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 163
2224
2224
3311
332
346
386
386
195
384
                                                                                                                                                           AA;
                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
 142
1164
1184
1184
120
133
133
134
118
118
118
184
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                      DOMAIN
TRANSMEM
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                                                                                                                                                                    955
                                                                                                                                              331
                                                                                                                                                                                            332 TrpLeuHisProAlaLeuPheAspPhePheThrTrpLeuGlyTyrLeuAsnSerLeuIle 351
                                                                                     --LeuPhePhe
                        GCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGGGAGCAG---
                                             275 AsnHisValGlnValLysLeuAla-----GluGlyValLeuGluArgLysArglle
                                                                     -----AAGGAGAGGCGAGCAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTG
                                                                                                                                     PURCH T., Palmier C., Colpaert F.C., Pauwels P.J.;

Murch T., Palmier C., Colpaert F.C., Pauwels P.J.;

Submitted (APR-1995) to the EMBL/Genbank/DDBJ databases.

-!- FUNCTION: This is one of the several different receptors for 5-
hydroxytryptemine (serotonin), a biogenic hormone that functions
as a neurotransmitter, a hormone, and a mitogen. The activity of
this receptor is mediated by G proteins that inhibit adenylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cyclase activity.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Strongest to the other 5HT-1 subtype receptors.
                                                                                                                                                                                                                   1070 AACCCCCTGATTTACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAG 1120
                                                                                                                                                                                                                                                                                                                                                                             Cricetulus griseus (Chinese hamster).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
5-hydroxytryptamine 1B receptor (5-HT-1B) (Serotonin receptor)
HTR1B.
                                                                                                                      CTGTGCTGGATCCCCTTCCTGACGGAACTCATCAGCCCACTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S54153; S54153.

InterPro; IPR002276; GPCR_Rhodpsn.
Pfam; PF00001; Trm1; 1.

PRINTS; PR00237; GFRRHODDPSN.
PROSITE; PS00237; GFRCHHODDPSN.
PROSITE; PS00237; GFRCHENT RECEP_F1_1; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family: Lipoprotein; Palmitate.

DOMAIN

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
C POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
260 LeuGlnGluGluArgSerHisAlaAlaGlyProPro--
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                                                                                                                                                                                                                                                                                           STANDARD;
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109
119
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|SerLeuAlaValThrAspLeuLeuValSerIleLeuValMetProValSerThrMetTyr 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 GAGCTGTCGACCGGGCGACGTCGCTGCTGGCCGGAGCCTGTGCCACGTGTGGATCTCC 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTCCGGTCACCATCCCGCGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 TCGACGGCCGTCTCGGACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 ThrVal---ThrGly---ArgTrpThrLeuGlyGlnValValCysAspPheTrpLeuSer 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 ProAsnLysThrGlyLysArgLeuThrArgAlaGlnLeuIleThrAspSerProGlySer 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 GICCIGGIGGIGACGCIGCIAGIGCIGCIGAICGCIGCCACTITCCIGIGGAACCIGCIG 226
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|ValLeuLeuValAlaLeuLeuAlaLeuIleThrLeuAlaThrThrLeuSerAsnAlaPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 ArgAlaAlaileMetileAlaLeuValTrpValPheSerileSerileSerLeuProPro
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---PhePheTrpArgGlnAlaLysAlaGluGluGluGluValLeuThrCysLeuValAsnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           407 TICGACGCCGGAGCCIGICITGIGCTGCCCCGCCGGGGCACGGGAACGIGGCGGCCAICGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      527 GCCICGTIGCTCAIGAICGCGCTCGCCCCGGGIGCCGICGGCGCTCAICGCCCTCGCGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    587 CTGCTCTTTGGCCGGGGCGAGGTGTGCGACGCTCGGCTCCAGCGCTGCCAGGTGAGCCGG
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                                                                                                                                        7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                   S-palmitoyl cysteine (Potential). BODC6211C2B6DECE CRC64;
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EXTRACELLULAR (POTENTIAL).
                       5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                       386
120
56
133
12
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Mismatches:
Indels:
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Matches:
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Transmembrane; Glycoprotein;

EXTRACELLULAR (POTENTIAL).

Lipoprotein; Palmitate

family;

2 (POTENTIAL). EXTRACELLULAR (POTENTIAL)

3 (POTENTIAL).

L \roughlam' .
CYTOPLASMIC (POTENTIAL)

(POTENTIAL)

CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
5 (POTENTIAL).

6 (POTENTIAL). EXTRACELLULAR (POTENTIAL) CYTOPLASMIC (POTENTIAL).

7 (POTENTIAL)

us-09-976-782-15.n2p.rsp

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G-protein
Multigene
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                                                                                                                                                            1051
                                                                                                                                                                                                                1012 TACTCCAATTCTTTCTTCAACCCCCTGATTTACACGCTTTTAACAAGAACTACAACAAT 1111
                                                                                                                                  334
                                                                                                                                                                                                                                           374
                          294
                                                                                                         997
                                                                                                                                                                                      335 IleCysLysAspAlaCysTrpPheHisMetAlaThrLeuAspPhePheAsnTrpLeuGly 354
                                                                    GTGGTGTTCACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGG
                         -----AspAlaLeu
                                                                                                         CTGAITGGCGTGTTTGTGCTGTGCTGGATCCCCTTCTTCCTGACGGAACTCATCAGCCCA
                                                                                                                                                            CTCTGT-----GCCTGCAGCCTGCCCCCATCTGGAAAAGCATATTTCTGTGGCTTGGC
                                                   GAGAGGCGAGCCATGATGGTGGGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                localization in motor control centers.";

Proc. Natl. Acad. Sci. U.S.A. 89:3020-3024(1992).

-!- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that inhibit adenylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mouse 5HT1B serotonin receptor: cloning, functional expression, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purkinje cells.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Strongest to the other 5HT-1 subtype receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cyclase activity.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Predominantly expressed in striatum and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plassat J.-L.,
                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
110-OCT-2003 (Rel. 42, Last annotation update)
5-hydroxytryptamine 1B receptor (5-HT-1B) (Serotonin receptor).
HTRIB OR SHTIB.
                         280 ProvalTyrValAsnGlnValLysValArgValSer----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maroteaux L., Saudou F., Amlaiky N., Boschert U.,
                                                                                                                                                                                                                                                                                                                                                    386 AA
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SEQUENCE FROM N.A.
MEDLINE=92212959; PubMed=1557407;
                                                                                                                                                                                                                                                                    1112 GCCTTCAAGAGCCTC 1126
                                                                                                                                                                                                                                                                                               375 AlaPheHisLysLeu 379
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                                                     896 CGGGAGCAGAAG
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                                                                                                                                                                                                                                                                                                                                                  SHIB MOUSE
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CIGCCGGGC 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 LeuAlaThrThrLeuSerAsnAlaPheValIleAlaThrValTyrArgThrArgLysLeu 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96
                                                                                                                                                                                                                                                                                                                                                                                                                                     38 GGCGTTGCCCTTGCCCTGGGACCCGAGACCAGCAGCGGGACCCCGAGACCCCAAGCCCGAGA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 SerIleMetHisLeuCysVallleAlaLeuAspArgTyrTrpAlaIleThrAspAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 GCTGCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCACCATCCCGCGGGGTCCGTGCCTTC
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                                                                                                                                                                                 (COLEMIAL).
N-LOUGHSMIC (GLUNAC. . .) (POTENTIAL)
N-LINKED (GLUNAC. . .) (POTENTIAL)
N-LINKED (GLUNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                             S-palmitoyl cysteine (Potential), 58F70FBEA770C0B3 CRC64;
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Mismatches:
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Matches:
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Percent Similarity:
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MGD; MGI:96274; Htrlb.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1, 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPCRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.

EMBL; Z11597; CAA77678.1; -. EMBL; M85151; AAA83221.1; -.

PIR; A42688; A42688

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284 GCCTCGACGGCCGTCTCGGACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCG 343
   neurotransmitter, a hormone, and a mitogen. The receptor is mediated by G proteins that inhibit
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Matches:
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Query Match:
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DOMAIN
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| ArgLysAlaThrLysThrLeuGlyIleIleLeuGlyAlaPheIleValCysTrpLeuPro 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||||||||:::
|PhePheIleIleSerLeuValMetProIleCysLysAspAlaCysTrpPheHisMetAla 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 IlePheAspPhePheAsnTrpLeuGlyTyrLeuAsnSerLeuIleAsnProlleIleTyr 365
                                  GluMetLeuAspCysPheValAsnThrAspHisValLeuTyrThrValTyrSerThrVal 210
                                                                                                                                                                                                                                                                                                                                                                                                           -----AspAlaLeuLeuGluLysLysLysLeuMetAlaAlaArgGlu 305
                                                                                               -GAG
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Neuropharmacology 36:513-524(1997).

-!- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions
CGGCTCCAGCGCTGCCAGGTGAGCCGGGAA----CCCTCCTATGCCGCCTTCTCCACCCGC
                                                                          GGCGCCTTCCACCTGCCGCTTGGCGTGGTGCCGTTTGTCTACCGGAAGATCTACGAGGCG
                                                                                                                                                   ----GGCCGCCGC---CGGAGAGCT
                                                                                                                                                                                    AlaArgSerArgIleLeuLysGlnThrProAsnLysThrGlyLysArgLeuThrArgAla
                                                                                                                                                                                                                       -- CCGTTGCCGGCCACCATGCAGGTGAGGTCCAAGGTA
                                                                                                                                                                                                                                                                                               AAGGAAGCACCTGATGAGGCT---GAAGTGGTGTTCACGGCACATTGCAAAGCAACGGTG
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Caviidae, Cavia.
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STRAIN=Hartley, TISSUE=Brain;
STRAIN=Hartley, TISSUE=Brain;
MEDLINE=971335; PubMed=8978753;
Wurch T., Palmier C. (Colpaert F.C., Pauwels P.J.;
"Sequence and functional analysis of cloned guinea pig and rat serotoon 5-HTID receptors: common pharmacological features with 5-HTID receptor subfamily.";
J. Neurochem. 68:410-418(1997).
                                                                                                                                                                                                                                                                                                                                                                      TCCTTCCAGGTGAGCGGGACTCCTGGCGGGAGCAGAAG------
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oĘ
                                                 cyclase activity.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Strongest to the other 5HT-1 subtype receptors.
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CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

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BY SIMILARITY.

R -> A (IN REF. 2)
activity
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InterPro; IPR000276; GPCR_Rhodpsn.
Pram; PR00001; 7tm 1; 1.
PRINTS; PR00237; GPRCRHODOPSN.
PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS0262; GPROTEIN RECEP F1 2; 1.
Multigene family.
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BXTRACBLIULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EXTRACELULAR (POTENTIAL).
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Non-endog Human 5-h

Abb56327 Aau79253 Aar45848 Aau75167

Ade56996

Human Human Human Amino aci Human ser

Serotonin Human 5-h

Aag62845 Aay28304 Aae00911 E

Sequence:

Run on:

Searched:

Amino aci

ser

Human Human

Aar43060

Abb56317

Non-endog

Abp72590 Abb58411

ser

Human Human

Abg73850

Abp81761 Ade40461

Murine 5H

Mouse

Human

Rat REC17

Aar58685

Human LP3 Drosophil Fruit fly Dog 5-HT Mouse isc Human ser

Abg74161 Abb57292

Aar15137

Aae38198

Serotonin

5-hydroxy

Aay28303 8 Aab47185 9 Abg73849 1

Human Human

Abp81762 Ade58162 Abb56318

HTR1A pro Human 5HT

Non-endog

Human

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Human; NOVX; cytostatic; antiarteriosclerotic; cardiovascular; lymphoma; antidiabetic; immunosuppressive; neuroprotective; gene therapy; cancer; cardiomyopathy; atherosclerosis; cell signal processing; diabetes; AIDS; metabolic pathway modulation; neoplastic; neurological disorder; asthma; adenocarcinoma; prostate cancer; uterus cancer; immune response; crohn; s disease; multiple sclerosis; Graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
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            AAU79252
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AAU75167
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ABP81761
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   Abb78809 Human NOV
Aac18654 Human G-p
Aam47211 Human NOV
Aam47212 Human NOV
Aac15638 Human G-p
Abg60235 Human G-p
Aar58686 Rat MR22
Ade56994 Rat Prote
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                      - protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes novel human proteins designated NOVX (where X is 1, 2a, 2b, 2c, 2d, 3, 4, 5, 6a, 6b, 7, 8, or 9). NOV1 is a tyrosine-protein kinase 6-like protein; NOV2a-d are keratin 4-like proteins; NOV3 is a collagen-like protein; NOV2a-d are keratin 1-like protein; NOV5 is a serotonin receptor-like protein; NOV6a and NOV65v are cold inducible glycoprotein 30-like protein; NOV7 is a matrilin-2-like protein; NOV9 is a leukocyte surface antigen (CD53)-like protein; and contains a tyrosine kinase-like protein. NOVX sequences have cytostatic, and interprotective activities, and can be used in gene therapy. The NOVX sequences can be used in therapeutics, particularly for treating, preventing or alleviating and human. These disorders include state in a subject, particularly a human. These disorders include cardiomyopathy, atherosclerosis, a disorder related to cell signal correspondences are also useful for determining the presence of or predisposition to a disease associated with altered levels of NOVX controlling useful in therapeutic or prophylactic applications for muchonic and interprotein and in the treatment of the resemble of the controlling of the description or nucleic acid, particularly cancer. The NOVX sequences are also expendent or prophylactic applications for especially useful in therapeutic or prophylactic applications for a disease associated with the treatment of for nucleic acid, particularly cancer. The NOVX sequences are especially useful in therapeutic or prophylactic applications for a disease associated with the treatment of the presence of the process or the pr
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Ellerman K;
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                                                                                                                                                                                                                                                        New NOVX polypeptides and polynucleotides, useful for treating or preventing a NOVX-associated disorder or a pathological state in a subject, particularly a human, e.g. cardiomyopathy, atherosclerosis,
                                                                                                                                      Spytek
                                                                                                                    Mishra V;
                                                                                                               ook JP, Lepley DM, Burgess CE, Mishra V
Padigaru M, Shimkets RA, Zerhusen BD, S
th V, Macdougall J, Stone D, Gunther E,
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18-JAN-2001; 2001US-0262455P.
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Gerlach V,
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                                                       CURAGEN CORP.
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Edinger S,
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321 IleProPhePheLeuThrGluLeuIleSerProLeuCysAlaCysSerLeuProProIle 340
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201 GluValCysAspAlaArgLeuGlnArgCysGlnValSerArgGluProSerTyrAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 PheSerThrArgGlyAlaPheHisLeuProLeuGlyValValValProPheValTyrArgLys
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                                                                   GluLeuValAlaAlaLeuAlaMetProProSerLeuAlaSerGluLeuSerThrGlyArg
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                                             GAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGA
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                                                                                                                                                                                                                                                                  IleProPhePheLeuThrGluLeuIleSerProLeuCysAlaCysSerLeuProProIle 331
 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; NOV5b; metabolic disorder; neurodegenerative disorder; immune disorder; haemacopoietic disorder; developmental disease; cancer; retinal disease; feeding disorder; vaccine; infection; gene therapy; neurological disorder; psychotic disorder; G-protein coupled receptor; cytostatic; antidiabetic; virucide; neuroprotective; nootropic; antidiabetic; antidigraine; anticorvalsant; neuroleptic; antipsoriatic; antiatheroscierotic; antimflammatory; anorectic; antiarthritic; antipsoriatic; antiatherosclerotic; antibacterial; fungicide; antiinflammatory; noorozoadide; antiulcer; hypertensive; hypotensive; serotonin receptor; chromosome 2.
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                                                                                                                                                                  272 ThralaHisCysLysAlaThrValSerPheGlnValSerGlyAspSerTrpArgGluGln
                                                            GCCACCATGCAGGTGAGGTCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGTGGTGTTC
                                                                                                                                              ACGCCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGGGAGCAG
TTCTCCACCCGCGCGCCTTCCACCTGCCGCTTGGCGTGCCGTTTGTCTACCGGAAG
                                                ATCTACGAGGCGGCCAAGTTTCGTTTCGGCCGCCGCCGGAGAGCTGTGCTGCCGTTGCCG
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25. .370
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2000US-0195343P.
2000US-0195005P.
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30-MAR-2000;
05-APR-2000;
06-APR-2000;
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The present invention provides the protein and coding sequences pf novel human G-protein coupled receptors, designated NOV1, NOV2, NOV3, NOV3, NOV5, N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
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Liu X, Patturajan M, Gusev VY;
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06-APR-2000; 2000US-019508BP.
10-APR-2000; 2000US-019592P.
11-APR-2000; 2000US-019655FP.
13-APR-2000; 2000US-0197081P.
14-APR-2000; 2000US-0197087P.
14-APR-2001; 2001US-0197525P.
29-MAR-2001; 2001US-00823187.
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Spytek KA,
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Best Local Similarity:
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The invention relates to isolated human G-protein coupled receptor (GCREC) polypeptides and their biologically active fragments. GCREC and protein is useful in treating a disease or condition associated with an increase or decrease in expression of functional GCREC. The GCREC's are useful in the diagnosis, treatment and prevention of cell proliferative disorders (cancer, leukaemia, melanoma); neurological disorders (stroke, epilepsy, Parkinson's disease, dementia, Alzheimer's disease); autoimmune inflammatory disorder (thyroiditis, haemolytic anaemia, AIDS, multiple solerosis); cardiovascular disorder (atherosclerosis, angina pectoris); gastrointestinal disorder (ulcer, cholelithiasis, gastroenteritis), metabolic disorders (diabetes); viral infections (herpes virus) and in the assessment of the effects of exogenous compounds on the expression of the nucleic acid and amino acid sequences. The present sequence is human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated human G-protein coupled receptor polypeptides and the use of these sequences in the diagnosis, treatment and prevention of diseases and in the assessment of exogenous compounds on the expression of the
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Khan FA, Patterson C, Lu DAM, Tx
Faul R, Yao MG, Yang J, Ramkumar J
dez R, Walsh RT, Borowsky ML, Thor
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Mismatches:
Indels:
'label= Mature_GCREC_8_protein
                 300. .318
/label= Transmembrane domain
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Matches:
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22-JUN-2000; 2000US-0213954P.
29-JUN-2000; 2000US-021699997-JUL-2000; 2000US-02189936P.
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21-JUL-2000; 2000US-0220141P.
                                                                                                                                 15-JUN-2001; 2001WO-US019275
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Griffin JA, Yue ..
'.. Y, Walia NK, Grau. ..
''c. Hernandez R, V
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                       GluValCysAspAlaArgLeuGlnArgCysGlnValSerArgGluProSerTyrAlaAla
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/label= Signal_peptide
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Ramkumar J, Au-Young J; / ML, Thornton M, He A;

Kallick DA; Tribouley CM; 20

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vascular disorder; infectious disease; anorexia; cancer; stroke; neurodegenerative disorder; Alzheimer's disease; acute brain injury; central nervous system disorder; depression; lung disorder; reproductive disorder; tissue disorder; thrombocytopaenia; migraine; angiogenesis; asthma; X-linked severe combined immunodeficiency; inflammation; autoimmune disorder; immune disorder; blood disorder; haematopoietic disorder; gastrointestinal disease; respiratory disorder; hepatitis; fertility; hypertension; arteriosclerosis; ischaemia; rheumatoid arthritis; Grave's disease; wound healing.
                      Human; NOVX; developmental disorder; endocrine disorder;
Human hydroxytryptamine receptor-like protein NOV8.
                                                                                                                                                                                                                                                    18-SEP-2000; 2000US-0233382P.
18-SEP-2000; 2000US-0233402P.
19-SEP-2000; 2000US-0233521P.
19-SEP-2000; 2000US-0233522P.
20-SEP-2000; 2000US-0233960P.
06-OCT-2000; 2000US-0233960P.
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2000US-0232676P.
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13-OCT-2000;
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(CURA-) CURAGEN CORP

Colman SD; Tchernev VT; G, Millet I; , Taupier RJ, Vernet CAM, T, Malyankar UM, Shenoy S, am M, Burgess CE, Smithson Gunther E, Ellerman K; Patturajan M, Syptek KA, Tchernev VT, Stone D, Padigaru M, Peyman JA, Mishra VS, Gorman L,

WPI; 2002-383182/41. N-PSDB; ABK71923 New cytoplasmic, nuclear, membrane bound and secreted NOVX polypeptides, useful for treating cancers and tumors, lung disorders, hematopoietic disorders, autoimmune diseases and immune disorders.

Claim 1 ; Page 60; 210pp; English.

The invention relates to an isolated NOVX polypeptide selected from NOV1a, NOV1a, NOV1a, NOV1a, NOV1a, NOV1a, NOV1a, NOV1a, NOV1b, NOV1a, NOV1b, NOV1a, NOV1b, NOV1a, NOV1b, Nov1

ABG60235 standard; protein; 380 AA.

30-JUL-2002 (first entry)

ABG60235;

AXXXEX XAXEX

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Key
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24-MAY-1995
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       appetite, thermoregulation, pain, perception, hormone secretion and sexual behaviour, immune disorders, haematopoietic disorders or other disorders related to cell signal processing and metabolic pathway modulation, gastrointestinal diseases, respiratory disorders, blood disorders, hepatitis, trauma, regeneration, viral, bacterial or parasitic infections, hyper- or hypo-thyroidism, endometriosis, fertility, hyperension, arteriosclerosis, ischaemia, haemolytic anaemia, wenner syndrome, rheumatoid arthritis, Grave's disease, wound healing, X-linked mental retardation, psychotic and neurological disorders and neuronal degeneration. The present sequence represents a NOVX protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The amino acid sequence of the novel rat serotonin receptor MR22. The gene encodes a protein of 370 amino acids. The protein contains 7 crassmenbrane domains (TMDs), a putative N-linked glycosylation site and 4 putative sites for kinase C phosphorylation. Serotonin regulates a wide range of sensory, motor and behavioural functions in the central nervous system (CNS). Serotonin receptors belong to at least two protein superfamilies: G-protein-associated receptors containing 7 TMDs superfamilies: G-protein-associated receptors presented in the patent represent prototypes that fall into three new serotonin subfamily classifications: 5-HT18-like (rat MR77 - AAQ72271 and human MR77 - AAQ72272), 5-HTS (subdivided into 5-HT5alpha, rat REC17 - AAQ7226) and 5-HT5beta, rat MR22 - AAQ72270) and 5-HT6 (rat REC20 - AAQ72273). The genes for the receptors were cloned by amplification based on conserved amino these sequences found in the TMDs. Degenerate primers were constructed to these sequences and used in two rounds of nested PCR amplification on a crat brain hypothalamic cDNA template. In the second round of amplification, degenerate primers corresponding to conserved residues con amplification, degenerate primers corresponding to conserved residues con Nully in indolalmine-binding receptors were used to amplify only those receptors. The resultant fragments were cloned into pBluescribt and their corresponding to obtain itill fangth clones. The nucleic acids and their corresponding to betain a tall thypothalamus and their corresponding to obtain and the second cound a catch their corresponding to obtain who can be a conserved and the conserved amplied and their corresponding to obtain and their conserved and the conserved 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a series of that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polypeptides, a method for producing a pharmaceutical composition, a method for identifying a compound that regulates its activity of one or more of the polypeptides or their antibodies. The polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more conducted sequence presented in experience presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed or protein in the printed or the sequence data for this patent did not form directly from WIPO at the specification, but was obtained in electronic form directly from wipo in the conduction of the sequence data for the sequence data for the specification of the specification of the sequence data for the specification of the specification of the sequence data for the sequence data for the sequence data for the seque
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N-PSDB; AAQ70264.
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Best Local Similarity:
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                                                                                                                                                                       Mus musculus
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27-MAR-1995
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184
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|LeuCysCysThrAlaSerIleTrpAsnValAlaAlaIleAlaLeuAspArgTyrTrpThr
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                                                                              CTAGTGCTGCTGATCGCTGCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCACCATCCCG
                                                                                                     99 ValLeuValAlaValLeuValMetProLeuSerLeuValSerGluLeuSerAlaGlyArg
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|176 AlaileThrTrpAlaLeuSerAlaLeuIleAlaLeuAlaProLeuLeuPheGlyTrpGly
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965 AFCCCCTFCTFCCFGACGGAACTCAFCAGCCCACTCTGFGCCFGCAGCCFGCCCCCCATC 1024
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176 AlaileThrTrpAlaLeuSerAlaLeuIleAlaLeuAlaProLeuLeuPheGlyTrpGly 195
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CTAGTGCTGCTGATCGCTGCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCACCATCCCG 244
                                                                                                                                                                     305 GAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGA 364
                                                                                                                                                                                                                                                      CGTCGGCTGCTGGGCCGGGAGCCTGTGCCACGTGTGGATCTCCTTTCGACGCCGGAGCCTGT 424
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                        79 ArgValArgAlaPheHisArgValProHisAsnLeuValAlaSerThrAlaValSerAsp
                                                                                                                                                                                                      99 ValLeuValAlaValLeuValMetProLeuSerLeuValSerGluLeuSerAlaGlyArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 ThrAlaArgArgArgAlaThrValThrPheGlnThrSerGlyAspSerTrpArgGluGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to transgenic animals, compositions and methods relating to the characterisation of gene function. The invention also relates to transgenic mice comprising mutations in 5-hydroxy-tryptophan (5-HT)5B receptor gene. The transgenic mice are useful for identifying an agent that modulates the phenotype such as increased depression or increased pain sensitivity. They are also useful for identifying potential therapeutic agents for the treatment of pain or depression and for evaluating a potential therapeutic agent capable of affecting a condition associated with a mutation in a 5-HT5B receptor gene. Transgenic animals of the invention are also useful for testing the efficacy of proposed genetic and pharmacological therapies for human diseases such as neurological, neuropsychological or psychotic illnesses. The present sequence is mouse 5-HT5B receptor protein
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                                                                                                Mouse; 5-hydroxytryptophan; 5-HT5B receptor; depression; transgenic; transgenic animal; phenotype; pain sensitivity; neurological disease; gene therapy; pharmacological; neuropsychological disease; analgesic; psychotic illness; receptor.
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Mismatches:
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83.64%
78.63%
67.43%
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21-DEC-2001; 2001US-0342472P.
28-MAR-2002; 2002US-00109532.
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                   (first entry)
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N-PSDB; AAD48747.
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Best Local Similarity:
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                                                               5-HT5B
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                  394 ArgLeuCysCysProAlaGlyLeuGlyAsnValAlaAlaIleAlaLeuGlyArgAspGly
                                                                                                                                      114 AlalleThrArgHisLeuGlnHisThrLeuArgThrArgSerArgAlaSerLeuLeuMet
                                                                                                                                                                                                434 IleAlaLeuAlaArgValProSerAlaLeuIleAlaLeuAlaProLeuLeuPheGlyArg
                                                                                                                                                                                                                                                             GlyGluValCysAspAlaArgLeuGlnArgCysGlnValSerArgGluProSerTyrAla
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                                                           TGTCTGTGCTCCCCCCCCCCCCTCGGGAACGTGGCGGCCATCGCCCTGGGCCGCGACGGG
                                                                                                                      GCCATCACACGCCACCTGCACCACGCACGCTGCGCACCCGCAGCCGCGCCTCGTTGCTCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; 5-hydroxytryptamine receptor 5A; HTR5A; serotonin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyAlaValLeuProGlyArgGlyProProPheSerValPheThrValLeuValValThr 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOOGCOSTCCTGCCGGGCCGAGGCCGCCCTTCTCTGTCTTCACGGTCCTGGTGGTGACG 181
                                                                                                                                                                                                                                                                                                                                           New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
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                            GPCR; guanosine triphosphate-binding protein coupled receptor;
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Matches:
Conservative:
Mismatches:
Indels:
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ID NO:610
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                                                                                                                                                                                                                                                                     Asai K, Akiyama Y,
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1296.50
83.33*
81.55*
Human GPCR protein SEQ
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N-PSDB; ADC86156.
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                                                                         Homo sapiens
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PheThrValArg---HisAlaThrValThrPheGlnProGluGlyAspThrTrpArgGlu 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 GlnLysGluGlnArgAlaAlaLeuMetValGlyIleLeuIleGlyValPheValLeuCys 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 ileTrpLysSerilePheLeuTrpLeuGlyTyrSerAsnSerPhePheAsnProLeuIle 337
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                                                                                                                                                                      203 PheSerThrValGlyAlaPheTyrLeuProLeuCysValValLeuPheValTyrTrpLys
                                                                                                                                                                                                                             ATCTACGAGGCGGCCAAGTTTCGTTTCGGC----CGCCGCCGGAGAGCTGTGCTGCCGTTG
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----GlnProGlnMetVal
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                                                               GAGGIGIGOGACGCICCAGCGCIGCCAGGIGAGCCGGGAACCCICCIAIGCCGCC
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                                                                                                                                                              The invention relates to single nucleotide polymorphisms in the gene encoding human 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A). A method for haplotyping the HTR5A gene in an individual comprises identifying the nucleotide at one or more polymorphic sites and etermining whether one of the copies of the gene is defined by one of the HTR5A haplotypes given in the specification or whether both copies are defined by a haplotype pair. This method is useful in genotyping, whereby all possible haplotype pairs can be assigned to specific genotypes. An association between a trial and a haplotype or haplotype or pair of the HTR5A gene can be identified by comparing the frequency of the haplotype pair in a population exhibiting the trait with the haplotype or haplotype frequency in the trait population. Computation, where a higher haplotype frequency in the trait population indicates the trait is associated with the haplotype or haplotype or haplotype and its corresponding DNA are used for studying the expression and function of HTR5A, and in screening for candidate drugs to treat diseases considered to HTRSA activity, such as neurological disorders, including expression and epilepsy. This sequence represents the human HTRSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244
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                                                Novel genetic variants of 5-Hydroxytryptamine (Serotonin) Receptor isogenes, useful for improving efficiency and reliability in drug development for treating neurological diseases.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                  Claim 31; Fig 4; 134pp; English.
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1063.50
72.98%
62.95%
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            N-PSDB; ABK50434
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New isolated antigenic peptides e.g., for G protein-coupled receptors (PGRS), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.
                                                                    Disclosure; Fig 1; 523pp; English
Brown JP;
Roush CL,
             WPI; 2003-046718/04.
                   N-PSDB; ABZ42828
Burmer GC,
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The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibody against a particular GPCR, and in the production of specific contribods and antibodies are useful for diagnosing and designing drugs for presence or absence of corresponding GPCRs rule antibodies are useful for diagnosing and designing drugs for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AlDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozcan or viral infections, of seteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriaeis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42223 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention

Sequence 357 AA;

357 Length: 2.73e-74 Alignment Scores: Pred. No.:

δλ	425 CIGIGCIGCCCGCCGCCTCGGGAACGIGGCGGCCATCGCCCTGGGCCGACGGGGCC 4	84
ΩD	rTrpSer 1	4
ζ	S ATCACACGCACCTGCAGCACACGCTGCGCACCCGCAGCCGCGCCCCCTTGCTCATGATC	4
ΩD	143 ileThrArgHisMetGluTyrThrLeuArgThrArgLysCysValSerAsnValMetile 1	62
δ	s gegetregecegegegegegeteareareagegege 6	4 0
αn	3 AlabeuinfirpAlabeuserAlavalileserbeuAlakrobeubeuknesiyirpsiy i	n o
δλ	605 GAGGTGTGCGACGCTCGGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCCTATGCCGCC 60	in
셤	183 GluthrTyrSerGluGlySerGluGluCysGlnValSerArgGluProSerTyrAlaVal 2	02
'n	665 TTCTCCACCCGCGGGCCTTCCACCGCGCTGGTGGCGTGGTGCTTTGTCTACCGGAAG 7	C)
qa	N	22
δλ	725 ATCTACGAGGCGGCCAAGTTTCGTTTCGGCCGCCGCGGAGAGCTGTGCTGCCGGTTG 71	81
qa	223 IleTyrLysAlaAlaLysPheArgValGlySerArgLysThrAsnSerValSerProlle 2	42
δλ	80	41
qa	243 SerGluAlaValGluValLySAspSerAlaLySGinProGinMetVal 2	28
ò	6	01
qq	259 PheThrValArgHisAlaThrValThrPheGlnProGluGlyAspThrTrpArgGlu 2	7
ζ	6	61
qu		6
δλ	Н	021
QC	298 TrplleProPhePheLeuThrGluLeulleSerProLeuCysSerCysAsplleProAla 3	17
λŏ	1022 AICHGGAAAAGCATATTTCTGTGGCTTGGCTACTCCAATTCTTTCT	081
qq	c.	37
ò	1082 TACACAGCTTTTAACAAGAACTACAATGCCTTCAAGAGCCTCTTTACTAAGCAG 1138	
qq	338 TyrThrAlaPheAsnLysAsnTyrAsnSerAlaPheLysAsnPhePheSerArgGln 356	
RESU AAE3	1.4 15	
a X	E38595 st	
A A C	AAE38595;	
TO	04-DEC-2003 (first entry)	
(임) 	man 5-hydroxytryptamine 5A (5-HT-5A) (serotonin rec	
¥ & §	man; urological disorder; urinary incontinence; gene therapy; can	
KW UI	uney unsoluer; overlarcive; oversemstrive braduer; uystunction; bradue ethra; overflow urinary incontinence; stress urinary incontinence; rivous system; prostatitis, benign prostatic hyperplasia; nephrotrophi	, i
ÆX	ceptor; GPCR.	
SO	Homo sapiens.	
N. A.	2003061573	
E 3	JUL-2003	
PF	16-JAN-2003; 2003WO-US001450.	
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1022 AICTGGAAAAGCATATTTCTGTGGCTTGGCTACTCCAATTCTTTCAACCCCCTGATT 1081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 IleTrpLysSerilePheLeuTrpLeuGlyTyrSerAsnSerPhePheAsnProLeuIle 337
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                                        GAGGTGTGCGACGCTCGGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCCTATGCCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGGCCACCATGCAGGTGAGGTCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGTGGTG
                                                                                                                                                                                                                                                                                                                                         TTCTCCACCCGCGCCCTTCCACCTGCCGCTTGGCGTGGTGCCGTTTGTCTACCGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerGluAlaValGluValLysAspSerAlaLys-------GlnProGlnMetVal
                                                                                                                  GCGCTCGCCCGGGTGCCGTCGCCGCTCATCGCCCTCGCGCCGCTGCTCTTTGGCCGGGGC
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present relates to a method for identifying a compound for treating urological disorders e.g., urinary incontinence including overactive/ oversensitive bladder, overflow urinary incontinence, stress urinary incontinence caused by dysfunction of the bladder, urethra or central or peripheral nervous system, prostatitis, benign prostatic hyperplasia, cancer of the prostate or kidney disorders. The method is also useful for modulating hyperplasia in a cell and treating a subject having a urological disorder. The invention is also used in gene therapy. The present sequence is human GPCR known as 5-hydroxytryptamine 5A (5-HT-5A) (serotonin receptor)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a compound for treating urological disorders, for example urinary incontinence by assaying the ability of the compound to modulate the nucleic acid expression or polypeptide activity.
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8 ThrSerPheSerLeuSerThrProSerProLeuGluThrAsnHisSerLeuGlyLysAsp
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Matches:
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                                                                                                                                                                                                                                                                                                               Karicheti V;
28-FEB-2002; 2002US-0360500P.
15-MAR-2002; 2002US-0365041P.
19-APR-2002; 2002US-0374663P.
14-AUG-2002; 2002US-0403468P.
27-SEP-2002; 2002US-0414262P.
21-OCT-2002; 2002US-0419986P.
05-NOV-2002; 2002US-0419986P.
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72.98%
62.95%
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Costigan M;
 Befort K,
D'urso D,
                      WPI; 2003-268312/26
                                   GENBANK; NP 076917
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Woolf
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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a gent to that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially compound for identifying a compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a compound that regulates the activity of one or more of the regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating contrivity in an animal of one or more of the polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating to polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating conjury (CCI) and spared nerve injury (CMI), in an animal (e.g. spinal segmental nerve injury (MIN)) in an animal (e.g. spinal segmental nerve injury (MIN)) in an animal (e.g. spinal segmental nerve injury (MIN)) in an animal (e.g. spinal segmental nerve injury (MIN)) in an animal (e.g. spinal segmental nerve injury (MIN)) in an animal (e.g. spinal segmental nerve injury (MIN) in an animal (e.g. spinal segmental nerve injury (MIN)) in an animal (e.g. spinal

Sequence 357 AA;

357 226 36 36 11 Matches: Conservative: Mismatches: Indels: 2.73e-74 1063.50 72.98% 62.95% 49.37% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: DB:

US-09-976-782-15 (1-1152) x ADE56996 (1-357)

ACCAGCAGCGGACCCGGGACCCCAAGCCCGAGAGGGATACTCGGTTCGACCCCGAGCGGC 124 ThrSerPheSerLeuSerThrProSerProLeuGluThrAsnHisSerLeuGlyLysAsp ω ð q

184 GCCGTCCTGCCGGGCCGAGGGCCGCCTTCTCTGTGTTCACGGTCCTGGTGGTGACGCTG

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CTAGTGCTGCTGATCGCTGCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCACCATCCCG 244 245 CGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTCTCGGAC 304

365 CGICGGCTGCTGGGCCGGAGCCTGTGCCACGTGTGGATCTCCTTCGACGCCGGAGCCTGT 424

484 TGGATCCCCTTCTTCCTGACGGAACTCATCAGCCCACTCTGTGCCTGCAGCCTGCCCCCC 1021 AICIGGAAAAGCATAIIICIGIGGCIIGGCIACICCAAIICIITCIICAACCCCCIGAII 1081 122 142 604 664 202 724 781 841 901 277 961 TACACAGCTITITAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGAG 1138 106 ArgTrpGlnLeuGlyArgArgLeuCysGlnLeuTrpIleAlaCysAspVal------|||| |GluThrTyrSerGluGlySerGluGluCysGlnValSerArgGluProSerTyrAlaVal CTGTGCTGCCCCGCCGGCCTCGGGAACGTGGCGGCCATCGCCCTGGGCCGCGACGGGGCC 318 IleTrpLysSerIlePheLeuTrpLeuGlyTyrSerAsnSerPhePheAsnProLeuIle GCGCTCGCCCGGGCCGTCGCCCTCATCGCCCTCGCGCCGCTGCTTTTGGCCGGGGC GAGGIGIGCGACGCICCGCCICCAGCCCAGGIGAGCCGGGAACCCIALIGCCGCC SerGluAlaValGluValLysAspSerAlaLys------GlnProGlnMetVal TTCACGGCACATTGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGGGAG CAGAAGGAGGCGAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTGC TICTCCACCCGCGCCGCCTTCCACCTGCCGCTTGGCGTGCTGCCGTTTGTCTACCGGAAG ATCTACGAGGCGGCCAAGTTTCGTTTCGGC----CGCCGGCGGAGAGCTGTGCCGTTG CCGGCCACCATGCAGGTGAGGTCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGTGGTG 425 123 485 143 545 183 203 223 782 243 605 999 725 842 902 962 1022 1082 338 à d à g à 셤 δ qq à g à qq ò g ò g ò 臼 à 셤 à g δ

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Q8sph2 sus scrofa
Q8mx83 aplysia cal
Q9n2d8 gorilla gor
Q9n2d9 pan troglod
Q9n2d7 pongo pygma
Q9n2b5 pan troglod
Q9n2b5 gorilla gor
P97842 rattus norv
Q9n2b4 pongo pygma
Q9n2b4 pongo pygma
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Q9n2b4 pongo
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Q98998 xenopus lae
Q9n263 sus scrofa
Q8sph2 sus scrofa
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Q9ng02 apis mellif
O77254 boophilus m
 986unl homo sapien
9n2b7 gorilla gor
Q99mb0 mesocricetu
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Q8buw7 mus musculu
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Q90wy4 brachydanio
Q7tla2 brachydanio
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O44198 apis mellif
Q8awel brachydanio
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sus scrofa
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Q9n297 gorilla gor
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Q925k7 mus
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S1:CC12PB.3 (Novel protein similar to human 5-hydroxytryptamine (Serotonin) receptor 5A (HTRSA)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corby N.; Submitted (FBB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AL772146; CAD61100.1; --
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO: GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IRF800276; GPCR_Rhodopsin.
FF00001; 7tm_1; 1.
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P97842
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Q8JG03
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Q925K7
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Q8MX83
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Cyprinidae; Dani
NCBI_TaxID=7955;
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                            Compugen Ltd.
                                                                     OM nucleic - protein search, using frame_plus_n2p model
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compug
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279 LeulleGlyValPheValLeuCysTrpIleProPhePheLeuAlaGluLeuIleIlePro
                                       AATTCTTTCTTCAACCCCCTGATTTACACAGCTTTTAACAAGAACTACAACAATGCCTTC
                          CTCTGTGCCTGCCCTGCCCCCCATCTGGAAAAGCATATTTCTGTGGCTTGGCTACTCC
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Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Cotton M., Phillips A., Tomlinson C.; "The sequence of Homo sapiens BAC clone RP11-5C23."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databa
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                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein HTR5A (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the EMBL/GenBank/DDBJ
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                                                                                                                                          339 ArgAsnLeuPheSerArgGlnArg 346
                                                                                                                                                                                                       PRT;
                                                                                                                             1118 AAGAGCCTCTTTACTAAGCAGAGA
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99063792; PubMed=9847074;
Sulston J.B., Waterston R.;
"Toward a complete human genome se
Genome Res. 8:1097-1108(1998).
                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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SEQUENCE FROM N.A.
Waterston R.;
Submitted (MAR-2002) t
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Submitted (FEB-2002)
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SEQUENCE FROM N.A.
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                             ATCGCCCTGGGGCCGCGACGGGCCATCACACGCCACCTGCACCACGCTGCGCACCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  521 AGCCGCGCCTCGTTGCTCATGATCGCGCTCGCCCGGGTGCCGTCGGCGCTCATCGCCCTC
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                                                                                                                                                                                                                                            TTCACGGTCCTGGTGACGCTGCTAGTGCTGCTGATCGCTGCCACTTTCCTGTGGAAC
                                                                                                                                                                                                                                                           49 LeuLeuValLeuValThrIleLeuArgValArgThrPheHisArgValProHisAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGCCCAAGTTTCGTTTCGGC---CGC
                                                                                                                                                                                                                                                                                            CTGCTGGTTCCGGTCACCATCCCGCGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 Serpro---LeuphedlyTrpdlydluThrTyrSerGluAspSerLeuAlaCysGlnVal
                                                                                                                                                                                                           GTGGCCTCGACGCCGTCTCGGACGACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTG
 PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN ERCEP F1 1; 1.
PROSITE; PS05026; G PROTEIN RECEP F1 2; 1.
SEQUENCE 346 AA; 39412 MW; BS54DIBC1E74413E CRC64;
                                                                            346
216
216
44
73
15
                                                                                                    Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                           |||| ::: |||||| :::
||leSerGlyGlySerGluSerGlyAsnLeuTyr
                                                                            Length:
Matches:
                                                                                                                                                                   (1-346)
                                                                                                                                                                  (1-1152) \times Q7ZZ32
                                                                        3.99e-62
1050.50
74.71%
62.07%
                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                   US-09-976-782-15
                                                                Alignment Scores:
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Best Local Similarity:
                                                                                                                                                                                                                                                    Percent Similarity
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                                                                                                                                                                                                                      Alignment Pred. No.:
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                                                                                                                                                                                                                                                                                                                                            ||||||||| ||| ::: |||||||
|LeuCysCysThrAlaSerIleTrpAsnValThrAlaIleAlaLeuAspArgTyrTrpSer 142
                                                                                                                                                                                                                                                                                       CGTCGGCTGCTGGGCCTGTGCCACGTGTGGATCTCCTTCGACGCCGGAGCCTGT 424
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163 AlaLeuThrTrpAlaLeuSerAlaVall1eSerLeuAlaProLeuLeuPheGlyTrpGly 182
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                                                                                                      27
                                                                                                                                                                                       99
                                                                                                                                                                            CGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTTCGACGGCCGTCTCGGAC
                                                                                                                                                                                                                          67 ArgValArgThrPheHisArgValProHisAsnLeuValAlaSerMetAlaValSerAsp
                                                                                                                                                                                                                                               305 GAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGA
                                                                                                  8 ThrSerPheSerLeuSerThrProSerProLeuGluThrAsnHisSerLeuGlyLysAsp
                                                                                                                                      CTAGTGCTGCTGATCGCTGCCACTTTCCTGTGGAACCTGCTTCCGGTCCACCATCCCG
                                                                                                                       GCCGTCCTGCCGGGCCGAGGGCCGCCTTCTCTGTCTTCACGGTCCTGGTGGTGACGCTG
                                                                                                                                                                                                                                                                                                                                                                        ATCACACGCACCTGCAGCACCACGCTGCGCACCCGCAGCCGCGCCTCGTTGCTCATGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluThrTyrSerGluGlySerGluGluCysGlnValSerArgGluProSerTyrAlaVal
                                                                                                                                                                                                                                                                                                          ArgTrpGlnLeuGlyArgArgLeuCysGlnLeuTrpIleAlaCysAspVal----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gorilla gorilla (gorilla).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Gorilla.
NCBI_TaxID=9593;
143
22
74
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2000 (TrEMBLrel. 15, Last sequence update) 5-hydroxytryptamine (Serotonin) receptor 1B. HTR1B.
         Conservative:
Mismatches:
Indels:
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 Matches:
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                                        Gaps:
                                                           US-09-976-782-15 (1-1152) x Q86UN1 (1-247)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TEBMBLrel. 15, Created)
01-0CT-2000 (TEBMBLrel. 15, Last seq
01-JUN-2003 (TEBMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  782 CCGCCCACCATGCAG 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerGluAlaValGlu 247
615.00
67.35%
58.37%
28.55%
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                   Similarity:
          Similarity:
                                                                               65
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                            Query Match:
DB:
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          Percent Sin
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ThrProAlaAsnTyrLeuIleAlaSerLeuAlaValThrAspLeuLeuValSerIleLeu 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 ValMetPro-----IleSerThrMetTyrThrValThrGlyArgTrpThrLeuGlyGln 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValValCysAspPheTrpLeuSerSerAsp-----IleThrCysCysThrAlaSer 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 IleLeuHisLeuCysVallleAlaLeuAspArgTyrTrpAlalleThrAspAlaValGlu 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               622
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PROBLEGE FROM N.A.

(E) STRAIN-gorilla-U1;

RA Kitano T., Kobayakawa H., Saitou N.;

RT "Silver Project.";

R. "Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 ProPro***ProAlaGlySerGluThrTrpValProGlnAlaAsnLeuSerSerAlaPro
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1127
63
1147
156
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PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 390 AA; 43565 MW; 37D54B95E3277FC3 CRC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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Length:

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                                              GCCTTCCACCTGCCGCTTGGCGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCC
                                                                                           AlapheTyrPheProThrLeuLeuLeulleAlaLeuTyrGlyArglleTyrValGluAla
                                                                                                                                                                                         ArgSerArgIleLeuLysGlnThrProAsnArgThrGlyLysArgLeuThrArgAlaGln
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

SUBMILLARITY: BELONGS TO FAMILY 1 OF G-PROTEIN (BY SIMILARITY).

EMBL, AF186554; AAK25827.1;

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin. .;

InterPro; IPR000276; GFCR_Rhodpsin.

Pfam; PP00001; Tul 1: 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Devor E.J., Devor R.M.;
"Cloning and sequencing the serotonin receptor SHTIB in the Hamster.";
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PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS00204; GPROTEIN RECEP F1 2; 1.
GPCOSITE; PS002062; GCPROTEIN.RECEP F1 2; 1.
SEQUENCE 386 AA; 43020 MW; 19F430C36F5CEB40 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Serotonin receptor 5HT1B.
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Alignment Scores:

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| LeuGluLysLysLysLeuMetAlaAlaArgGluArgLysAlaThrLysThrLeuGlyIle 314
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ValLeuLeuValAlaLeuLeuAlaLeuIleThrLeuAlaThrThrLeuSerAsnAlaPhe 65
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|SerLeuAlaValThrAspLeuLeuValSerIleLeuValMetProValSerThrMetTyr
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Query Match:
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980 ACGGAACTCATCAGCCCACTCTGT-----GCCTGCAGCCTGCCCCCCCATCTGGAAAGC 1033
                                                   AspLeuPheileAlaLeuAspVal------LeuCysCysThrSerSerIleLeuHis 126
                    392 CACGIGIGGAICTCCIICGACGCCGGAGCCIGICIGIGCIGCCCCGCCCGGCCICGGGAAC 451
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01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
5-hydroxytryptamine 7 receptor.
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                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                      van den Berg I., Versteeg S., van Oost B.; "Isolation and characterization of the canine serotonin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                     gene (HTRIA).";
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX134445; ANG044.1;
GO, GO:0016021; C:integral to membrane; IEA.
GO, GO:0004897; F:receptor activity; IEA.
GO; GO:0001894; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; F:G-protein coupled receptor protein signalin.
InterPro; IPR000276; GPCR_Rhodpsn.
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Conservative:
Mismatches:
Indels:
Gaps:
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
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Canis familiaris (Dog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAGCTGTGCCGTTGCCGGCCACCATGCAGGTGAGGTCCAAGGTAAAGGAAGCACCT 823
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Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
Aplysioidea; Aplysiidae; Aplysia.
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                                                                                                                              ProLeuLeulleLeuGlyAsnGluHisMetThrAsnGlyGlnProSerCysSerValCys
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                                                                 CCGCTGCTCTTTGGCCGGGGGGGGGTGTGCGACGCTCGGCTCCAGCGCTGCCAGGTGAGC
                                                                                                                                                                                                CGGGAACCCTCCTATGCCGCCTTCTCCACCCGCGCGCCCTTCCACCTGCCGCTTGGCGTG
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J. Neurosci. 18:5586-5531[1938].

J. Neurosci. 18:5586-5531[1938].

J. SIMILARITY BELOATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARI SENELLY BELOATION: INTEGRAL MEMBRANE PROTEIN COUPLED RECEPTOR GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

GO; GO:0001584; F:rhodopsin-like receptor protein signalin.

InterPro; IPR000275; GPCR_Rhodopsin.

PFam; PF00001; 7tm_1; 1.
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Angers A., Storozhuk M.V., Duchaine T., Castellucci V.F.
DesGroseillers L.;
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                                                                                                                                                                                            Pictrantonio P.V., Jagge C.L.;
Pictrantonio P.V., Jagge C.L.;

"Cloning of a serotonin receptor 5HT7-like cDNA from mosquito Aedes agypti Clopterat Culicidae) excretory and respiratory systems.";

"Cloning of a serotonin receptor 5HT7-like cDNA from mosquito Aedes agypti Clopterat Culicidae) excretory and respiratory systems.";

submitted (JAN-2001) to the BMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

C. -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-ROTEIN COUPLED RECEPTORS.

BMBL; AR296125; AAG49292.1;

CO; GO:00016021; C:integral to membrane; IEA.

CO; GO:0001801; P:receptor activity; IEA.

CO; GO:0001804; P:rrodopsin-like receptor activity; IEA.

CO; GO:0001804; P:rrodopsin-like receptor protein signalin. . .; IEA.

RO; GO:0001186; P:G-Protein coupled receptor protein signalin. . .; IEA.

RRINTS; PRO00237; GPCRRHODOPSN.

R PRINTS; PRO00237; GPROTEIN RECEP FI.1; 1.

RROSITE; PSO0237; GREOPERIN RECEP FI.1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .; IEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 ArgLeuThrProThrSerSer-----ThrSerSerLeuLeuAspGluLeuGlyGly
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                                     Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Aedes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCGCTAGCCTTTCAGTGGCCACCGCCGCGTTGCCCTTGCCCTGGGA-
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      aegypti (Yellowfever mosquito)
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30.81%
20.17%
                                                                                                                                                                           SEQUENCE FROM N.A.
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Best Local Similarity:
                                                                                                          NCBI_TaxID=7159;
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Pred. No.:
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| 11 | |||||||:::
| ArgGluLysMetGluMetAlaArgGluArgLysValTrpLeuArgValLeuGLyIleIle 416
                  GlyGluTrpSerThrArgArgProAlaGlySerLysProAspSerHisValValGlnHis 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Silver Project.";
"Silver Project.";
"Silver Project.";
"Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

REMBL; AB041405; BA49490.1; -.

RO; GO:0004872; F:receptor activity; IEA.

GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.

RO; GO:0001884; F:rhodopsin-like receptor protein signalin. .; IEA

RO; GO:0001186; P:G-protein coupled receptor protein signalin. .; IEA

RO; GO:0001186; P:G-protein coupled receptor protein signalin. .; IEA

RO; GO:0001186; P:G-protein coupled receptor protein signalin. .; IEA

ROS: GO:0001186; P:G-PROTEIN RECEP FI_1; 1.

ROSITE; PS00237; GPCRRHODOPSN.

RROSITE; PS00237; GPCRRHODOPSN.

RROSITE; PS00237; GPCRRHODOPSN.

RROSITE; PS00237; GPCRRHODOPSN.

RROSITE; PS00262; GPROTEIN RECEP FI_2; 1.

ROSICE A22 A4; 46154 MW; 012335E0403F1B90 CRC64;
                                                                               357 ThrAspArgProSerMetHisLeuLeuAlaSerProTyrProValGlnGluProArgSer
                                                                                                                                             377 ArgPheGlnGlnArgHisGlnLysThrGluThrHisArgGlnArgValValPheArg
                                                                                                                                                                                                                                                             417 ThrGlyAlabheValValCysTrpLeuProPhePheValValAlaValLysProMet
                                                                                                                                                                                                                                                                                                                                   437 CysGlyThrProCysAspMetProSerTyrValTyrSerLeuPheLeuTrpLeuGlyTyr
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
NCBI_TaxID=9593;
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120
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Last sequence update)
Last annotation update)
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Kitano T., Kobayakawa H., Saitou N.;
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|PheAsnLysIlePheLeuArgArg
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432.00
45.30%
28.92%
20.06%
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Best Local Similarity:
Query Match:
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|GlulleSerIle----HisTrpPheLeuGlyAsnAlaValCysAspMetTrpValSer 155
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                                                                                                                                                                                                                                                             GICCIGGIGGIGACGCTGCTAGTGCTGCTGATCGCTGCCACTTTCCTGTGGAACCTGCTG 226
                                                                                                                                                                                                                                                                                                                         GTTCCGGTCACCATCCCGCGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCC 286
                                                                                                                                                                                                                                                                                                                                                                                        TCGACGGCCGTCTCGGACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGT 346
                                                                                                                                                                                                                                                                                                                                                                                                                    SerLeuAlaValThrAspLeuLeuValAlaValLeuValMetProLeuSerLeuIleTyr 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PheAspArgTyrTrpAlaValSer---AsnIleAspTyrValArgSerArgAsnAlaArg 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGGAACCCTCCTATGCCGCCTTCTCCACCCGCGGCGCCTTCCACCTGCCGCTTGGCGTG 703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGCTGTCGACCGGGCGACGTCGGCTGCTGGCCGGAGCCTGTGCCACGTGTGGATCTCC
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PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 492 AA; 56261 MW; 24F0044CA94901B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA-----GCAACGGTGTCCTTCCAGGTGAGCGGGGAC----
                                                                                                               492
119
63
121
125
                                                                                                               Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                              Indels:
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27.80%
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"Direct Submission.";

"Direct Submission.";

"Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

"Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

"Is SUBMITARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

"EMBL; U15167; AAB66360.1; -

"REMBL; AC084154; AAK29875.2; -

"REMBL; AC084154; AAK29875.2; -

"REMBL; AC084154; AAK29875.2; -

"REMBL; AC084154; Excepton membrane; IEA.

"GO; GO: 0004872; F: receptor activity; IEA.

"GO; GO: 0004875; F: receptor activity; IEA.

"GO; GO: 000186; F: Receptor activity; IEA.

"GO: GO: 000186; F: Receptor activity; IEA.
                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP FI 1; 1.

PROSITE; PS50262; G PROTEIN RECEP FI 2; 1.

Hypotherical protein; G-protein coupled receptor; Receptor; Transmembrane.
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                 CCCTTCTTCCTGACGGAACTCATCAGCCCACTCTGT
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"Molecular cloning and functional expression canorhabditis elegans.";
J. Mol. Neurosci. 0:0-0(1997).
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Science 282:2012-2018(1998).
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01-JAN-1998 (TrEMBLrel. 05,
01-OCT-2003 (TrEMBLrel. 25,
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26 ThrGlyIleSerAspValThrPheSerTyrGlnValIleThrSerLeuLeuGlyThr
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86 SerValLeuValLeuPro-----MetAlaAlaLeuTyrGlnValLeuAsnLysTrpThr
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221 AlaAlaArgPheArgIleArgLysThrValLysLysValGluLysThrGlyAlaAspThr
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ProGlyGlnGlyAsnAsnThrThrSerProProAlaProPheGluThrGlyGlyAsnThr
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	DD 296 ThrAsnberileLysAsnProbroArgHisAsnGluberSerSerSerAlaSerGluGiu 315 Qy 827 GAGGCTGAAGTGGTGTTCACGGCACATTGCAAAGGGTGCCTTCCAGGTG 880	536 ILEASDGLUGIUABUGIYALGSELLYBELUGIYLLEYGALLYBALGALGALGALGALGALGALGALGALGALGALGALGALGA	356 GluSerAsnGluMetLysArgGluArgLysAlaTrpArgThrLeuAlaIleIleThrGly	Db 376 ThrPheValAlaCysTrpThrProPhePheLeuValSerIleTyrArgProIleCysGly 395	OY 1007 TGCAGCCTGCCCCATCTGGAAAAGCATATTTCTGTGGCTTGGCTACTCCAATTCTTTC 1066	1067 TTCAACCCCTGA ::: 416 LeuAsnProlleI		RESULT 10 QBBZP1 ID OBBZP1 AC OBBZP1: PRELIMINARY, PRT; 421 AA.			N NEL TAXID=10090; RN (1) RP SEQUENCE FROM N.A. RC STRAIN=CSTBL/6J; TISSUE=Diencephalon;		60,770 Full-len Nature 420:563- EMBL; AK034017; MGD; MGI:96273;		DR PEAM; PEOUS 1, 7 PEOUS 1, 1. 1. DR PRINTS; PRO0237; GPCRENDODOSN. DR PROSITE; PS00237; G PROTEIN RECEP F1 1; 1. DR PROSITE; PS00262; G PROTEIN RECEP F2; 1.	ignment Scores: 9.69e-21 Length: 421	Score: 431.00 marches: 11/ Percent Similarity: 45.50% Conservative: 65 Best Local Similarity: 29.25% Mismatches: 122 Onery Match: 20.01% Indels: 96	11 Gaps:
SEQUENCE 445 AA; 50141 MW; ED6D8EB88ABC7EC0 CRC64;	Alignment Scores: 9e-21 Length: 445 Score: 431.50 Matches: 135 Percent Similarity: 44.24\$ Conservative: 61 Best Local Similarity: 30.47\$ Mismatches: 156 Query Match: 5 Gaps: 13	-09-976-782-15 (1-1152) x O18512 (1-445)	47 CTTGCCCTGGGACCCGAGACCAGCAGACCCGAGCCCGAGAGGGAGAGATACTC 106	107 GGTTCGACCCCGAGGGGCGCCGTCTGCCGGGCCGAGGGCCGCCTTC 154	TCTGTCTTCACGGTCCTGGTGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT	197 ATCGCTGCCACTTTCCTGTGGAACCTGCTGGTGCGTTCCGGTCCCGTGGCCGTGCTCCGTGCTCCTGTTGCTGC	257 TTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTCTCGGACGACGACGACGACGACGACGACGACGACGACGACGA		374 CTGGCCCGGAGCCTGTGCCACGTGGATCTCCTTCGACGCGGGGCCTGTCTGT	Oy 434 CCCGCCGGCCTCGGGAACGTGGCCGTCGCCCTGGGCCGCGACGGGGCCATCACACGG 493 Db 137 ThralaSerIleLeuHisLeuValalaIleAlaLeuAspArgTyrTrpSerIleThrAsp 156	OY 494 CACCTGCAGCACGCGCACCCGCAGCCGCGCCTCGTTGCTCATGATCGCGCTCGCC 553	Qy 554 CGGGTGCCGTCGGCGCTCATCGCCCTCGCGCTGCTTTGGCCGGGCGAGGTGTGC 613	Qy 614 GACGCTCGAGCGCTGCCAGGTGAGCCGGGAACCCTCCTATGCCGCC 664	Qy 665 TTCTCCACCCGGGGGCGCTTCCACCTGCCGCTTGGCGTGGTGCTTTGTCTACCGGAAG 724	Qy 725 ALCTACGAGGCGAGGTTTCGGCCGCCGCCGGAGAGCTGTGCTG 775	Qy 776 CCGTTQCCG	Oy 808	809GTABARGGARGCACCTGATGATGAT

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TGCAGCCTGCCCCCCATCTGGAAAAGCATATTTCTGTGGGCTTGGCTACTCCAATTCTTTC 1066
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Matches:
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                                                                                                                                                                                                            Pongo pygmaeus (Orangutan).
                                                                                                                                                                                     Serotonin receptor 1A. HTRIA.
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                                                                                         GlyAsnAlaCysvalvalAlaAlaIleAlaLeuGluArgSerLeuHisAsnValAlaAsn 72
                      TICACGGICCIGGIGGIGACGCIGCIAGIGCIG-----CIGALCGCIGCCACITICCTG
                                  275 AACTIGGIGGCCICGACGGCCGICICGGACGAACTAGIGGCAGCGCIGGCGAIGCCACCG
                                                                                                                              335 AGCCTGGCGAGTGAGCTGTCGACCGGGCGACGTCGGCTGCTGGGCCGGAGCCTGTGCCAC
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|FeuleuleumetleuValleuTyrGlyArgIlePheArgAlaAlaArgPheArgIleArg
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168 SerlleProProMetLeuGlyTrpArgThrProGluAspArgSerAsnProAsnGluCys
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A Kitano T., Kobayakawa H., Saitou N.;

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

C. -: SIMILARITY BELOGGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

REMBL, AB041406; BAA94491.1; -

R GO; GO:00016021; C:integral to membrane; IEA.

R GO; GO:0001864; F:receptor activity; IEA.

R GO; GO:000186; F:receptor activity; IEA.

R GO; GO:000186; F:receptor activity; IEA.

R GO; GO:0001186; F:receptor; Receptor; Transmembrane.

R PROSITE; PSO262; G-PROTEIN RECEP FI.; 1.

R PROSITE; R-SCEPTOR ACTIVE RECEP FI.; 1.
||| :::||| ::: ||| 375 CysHisMetProGluLeuGlyAlaIlelleAsnTrpLeuGlyTyrSerAsnSerLeu
                                                                                                                                        1067 ITCAACCCCCTGATTTACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTC
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pongo.
NCBI_TaxID=9600;
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SEQUENCE FROM N.A.
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|GluArgLysThrValLysThrLeuGlyIleIleMetGlyThrPheIleLeuCysTrpLeu 359
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            493
                                                           ThrSerSerIleLeuHisLeuCysAlaIleAlaLeuAspArgTyrTrpAlaIleThrAsp 140
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                                                                                                          141 ProlleAspTyrValAsnLysArgThrProArgArgAlaAlaAlaLeuileSerLeuThr 160
                                                                                                                                                                                                                          CGCGGCGCCCTTCCACCTGCCGCTTGGCGTGCTGCCGTTTGTCTACCGGAAGATCTACGAG 733
                                                                                                                                                                                                                                                                                                                                       241 HisHisGlyAlaSerProAlaProGlnProLysLysSerValAsnGlyGluSerGlySer 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerLysGluHisLeuProLeuProSerGluAlaGlyProThrProCys---AlaProAla 319
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|ValArgGInGlyAspAspGlyAlaAlaLeuGluValIleGluValHisArqValGlyAsn
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                                                                                      CACCTGCAGCACACGCTGCGCACCCGCAGCCGCGCCTCGTTGCTCATGATCGCGCTCGCC
                                                                                                                                                                               GACGCTCGGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCCTATGCCGCCTTCTCCACC
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PheGlyAlaPheTyrIleProLeuLeuLeuMetLeuValLeuTyrGlyArgIlePheArg
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| AlaAlaArgPheArglleArgLysThrValLysLysValGluLysThrGlyAlaAspThr
                                                                                                                                                                                                                                                                                                                                                                                  261 ArgAsnTrpArgLeuGlyValGluSerLysAlaGlyGlyGlyLeuCysAlaAsnGlyAla
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                                                                                                                                  CGGGTGCCGTCGGCGCTCATCGCCCTCGCGCCGCTCTTTGGCCGGGGCGAGGTGTGC
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GTAAAGGAAGCACCTGATGAGGCTGAAGTG---GTGTTCACGGCACAT-----
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TyralaTyrPheAsnLysAspPheGlnAsnAlaPheLysLysIle
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Last sequence update) Last annotation update)

Created) PRT;

01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2003 (TrEMBLrel. 24,

Q9N298; 01-OCT-2000

Serotonin receptor 1A. HTR1A.

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                                                                                                                                                                                                                                                                                       C. -: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

C. -: SIMILARITY: BELOATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

REMEL; ABO41404; BA494891;

CO; GO: 0016021; C:integral to membrane; IEA.

RO; GO: 0016021; F:receptor activity; IEA.

RO; GO: 0001884; F:rhodopsin-like receptor activity; IEA.

RO; GO: 0001884; F:rhodopsin-like receptor protein signalin. . .; IEZ

RO; GO: 0001886; P:G-protein coupled receptor protein signalin. . .; IEZ

RO; GO: 000186; P:G-protein coupled receptor protein signalin. . .; IEZ

ROS; GO: 000186; P:G-protein Coupled receptor; Receptor protein signalin. . .; IEZ

ROSITE: PS00237; GPCRRHODOPSN.

RROSITE: PS00237; GPCRRHODOPSN.

RROSITE: PS00237; GPCRRHODOPSN.

RROSITE: PS00226; G-PROTEIN RECEP F1 1; 1.

G-protein coupled receptor; Receptor; Transmembrane.

G-protein coupled receptor; Receptor; Transmembrane.
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|LeuGlyGlnValThrCysAspLeuPheIleAlaLeuAspVal-----LeuCysCys
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                                    Euteleostomi;
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troglodytes (Chimpanzee).
nryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
nalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                            Kitano T., Kobayakawa H., Saitou N.;
"Silver Project.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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Mismatches:
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19.87%
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                                    Eukaryota, Metazoa,
Mammalia, Eutheria,
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|AlaSerLeuAlaValThrAspLeuLeuValSerIleLeuValMetPro-----IleSer 106
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                                                                                                                                                                                                                                                                                                                                                                                                          GCGGCCCCTCCTGCCGGCCCGAGGC-----CGCCCTTCTCTCTGTC----TTC 163
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ProLeuProAlaSerSerGlnThrArgLeuSerGlnAlaAsnLeuSerAlaAlaPro--- 29
                                                                                                                                                                                                                                                                                                                                                                                                                                              ---SerGlnAsnCysSerAlaGluGlyTyrIleTyrGlnAspSerIleAlaLeuProTrp 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGAGACCAGCAGCGGACCCGGGACCCCCAAGCCCGAGAGGGATACTCGGTTCGACCCCGA
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|PheValIleAlaThrValTyrArgThrArgLysLeuHisThrProAlaAsnTyrLeuIle
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Pfam; PF00001; 7tm 1; 1.

PRINTS; PR00237; GPCRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.

PROSITE; PS50262; GPROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Receptor; Transmembrane.

SEQUENCE 390 AA; 43417 MW; 08EB9731C84E7474 CRC64;
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Matches:
Conservative:
Mismatches:
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426.50
49.74%
32.38%
19.80%
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cal Similarity:
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-!- SUBCELLUIAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AF186226; AAG15397.1; --
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:b-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPCR_Rhodpsn.
                                      CGCGGCCTTCCACCTGCCGCTTGGCGTGCCGTTTGTCTACCGGAAGATCTACGAG
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  181 ArgSerAspProAspAlaCysThrIleSerLysAspHisGlyTyrThrIleTyrSerThr
                                                                          PhedlyAlaPheTyrIleProLeuLeuLeuMetLeuValLeuTyrGlyArgilePheArg
                                                                                                                   GCGGCCAAGTTTCGTTTTCGCCCGCCGCCGGAGAGCTGTGCTGCCGTTGCCGGCCACC---
                                                                                                                                                       AlaAlaArgPheArgIle-----ArgLysThrValLysLysValGluLysThrGly
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SEQUENCE FROM N.A.
STRAIN-breed Landrace x Yorkshire; TISSUE-Brain cortex;
Bhalla P., Xiaoqian M., Saxena P.R., Sharma H.S.;
"Molecular cloning and tissue distribution of porcine 5-HTIB
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Cetartiodactyla; Suina; Suidae;
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Eukaryota; Metazoa; Chordata; Cran Mammalia; Eutheria; Cetartiodactyl:
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                  ---GluValLeuGlnAlaLeu 34
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The FANTOM Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length CDMAs.";
Nature 420:563-73(2002).
BAGIS MAI:96276; Hrid.
MGD; MGI:96276; Hrid.
GO; GO:001684; Frihodopsin-like receptor activity; IEA.
GO; GO:0001884; Frihodopsin-like receptor activity; IEA.
GO; GO:000186; Fichpopsin-like receptor protein signalin. .;
InterPro: IRR000276; GFCR_Rhodopsn.
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Mus musculus (Mouse).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

NCBI_TaxID=10090,
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PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS0024; G PROTEIN RECEP F1 2; 1.
SEQUENCE 374 AA; 41593 MW, 2FE947DF7DBEF14D CRC64;
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1119
67
150
53
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                 SerProvalTyrValAsnGlnValLysValArgValSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5-hydroxytryptamine 1D receptor.
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423.50
47.81%
30.59%
19.66%
                                                                              TGGCGGGAGCAGAAG
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                           283
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GAAGCACCTGATGAGGCT

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1067 ITCAACCCCCTGAITTACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTC 1126
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148 ArgThrProArgArgArgAlaAlaAlaLeuIleSerLeuThrTrpLeuIleGlyPheLeuIle 167
                                                                                                                                      288 AlaThrLeuGluValIleGluValHisArgValGlyAsnSerLysGlyHisLeuProLeu 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 IleLeuCysTrpLeuProPhePheIleValAlaLeuValLeuProPheCysGluSers8r 374
                                                                                  168 SerIleProProMetLeuGlyTrpArgThrProGluAspArgSerAsnProAsnGluCys 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 ProserGluserGlyAlaThrSerTyrValProAlaCysLeuGluArgLysAsnGluArg 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    893 IGGCGGGAGCAGAAGGAGGCGAGCCAGCCATGATGGTGGGAATTCTGATTGGCGTGTTT 952
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|LeuAsnProValIleTyrAlaTyrPheAsnLysAspPheGlnAsnAlaPheLysLysIle 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||| :::||| :::||375 CysHisMetProGluLeuGlyAlaIlelleAsnTrpLeuGlyTyrSerAsnSerLeu
                                                  GCCCTCGCGCCGCTGCTCTTTGGCCGGGGGGGGGTGTGCGACGCTCGGCTCCAGCGCTGC
                                                                                                                     CAGGTGAGCCGGGAACCCTCCTATGCCGCCTTCTCCACCCGCGCGCCCTTCCACCTGCCG
                                                                                                                                                                                                                                                                                    228 LysThrValLysLysValGluLysLysGlyAlaGlyThrSerPheGlyThrSerSerAla
                                                                                                                                                                                                                                                                                                                                                    248 ProProProLysLysSerLeuAsnGlyGlnProGlySerGlyAspCysArgArgSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                    268 GluAsnArgAlaValGlyThrProCysAlaAsnGlyAlaValArgGlnGlyGluAspAsp
                                                                                                                                                                                     CTTGGCGTGGTGCCGTTTGTCTACCGGAAGATCTACGAGGCGGCCAAGTTTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 AACTIGGIGGCCTCGACGCCGTCTCGGACGAACTAGIGGCAGCGCTGGCGATGCCACCG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCCTGGCGAGTGAGCTGTCGACCGGGCGACGTCGGCTGCTGCGCGGAGCCTGTGCCAC 394
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---MetAlaAlaLeuTyrGlnValLeuAsnLysTrpThrLeuGlyGlnValThrCysAsp 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIGIGGAICTCCTTCGACGCCGGAGCCTGTGTGCTGCCCGCCGCCGCCTCGGGAACGTG 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGGCCATCGCCCTGGGCCGCGACGGGCCATCACACGGCACCTGCAGCACACACGCTGCGC 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CysAlaileAlaLeuAspArgTyrTrpAlaileThrAspProIleAspTyrValAsnLys 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||:::
33 PheSerTyrGlnVallleThrSerLeuLeuLeuGlyThrLeullePheCysAlaValLeu 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001186; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001186; F:rhodopsin-like receptor protein signalin. . .; IEA.
Interpro; IRM000276; GPGR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; GPROTEIN_RECEP_F1 1; 1.
PROSITE; PS00245; G_PROTEIN_RECEP_F1 2; 1.
SEQUENCE 421 AA; 46175 MW; 74F519DF7CCOC7AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyAsnAlaCysValValAlaAlaileAlaLeuGluArgSerLeuGlnAsnValAlaAsn 72
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUB-Cortex, and Hippocampus;
MFDLINE-2234683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK043668; BAC31611.1; -.
EMBL; AK043668; BAC31611.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 TGGAACCTGCTGGTTCCGGTCACCATCCCGCGGGTCCGTGCCTTCCACCGCGTGCCGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421
116
65
123
96
                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                   421
AspPheArgGlnAlaPheGlnLysVal 367
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423.00
45.25%
29.00%
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                                                                 PRELIMINARY;
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MGD; MGI:96273; Htrla.
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Sequence:

receptor

receptor

receptor receptor receptor

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A;Cross-references: EMBL:X69867; NID:g288735; PIDN:CAA49501.1; PID:g288736
C;Superfamily: octopamine receptor type I
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: 148231
R;Matches, H: Boschert, U.; Amlaiky, N.; Grailhe, R.; Plassat, J.L.; Muscatelli, F.;
Mol. Pharmacol. 43, 313-319, 1993
A;Title: Mouse 5-hydroxytryptamine5A and 5-hydroxytryptamine5B receptors define a new A;Reference number: 148231; MUID:93196607; PMID:8450829
                                                                                receptor
receptor
                                                                                                                                               serotonin receptor
                                                                                                                                                            serotonin receptor
                                                                                                                                                                         G protein-coupled serotonin receptor
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alpha-2A-adrenergi
alpha-2-C2 adrener
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alpha-1A adrenergi
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                                                      serotonin serotonin
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                                          serotonin
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298
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Mismatches:
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A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-370 <RES>
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Matches:
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A48881
A47174
I77467
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S26048
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A47519
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A47385
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A45121
A40491
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S28221
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JC1525
A38731
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DYHUD2
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Percent Similarity:
Best Local Similarity:
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-MODEL=frame+ n2p.model -DEV=xlp
-Q=Cggl2 1/USFTO spool_p/US09976782/runat_31082004_115951_10328/app_query.fasta_1.1351
-Q=Cggl2 1/USFTO spool_p/US09976782/runat_31082004_115951_10328/app_query.fasta_1.1351
-DB=FIR 78 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1.0GPEXT=0
-UNITS=Eits -START=1 -END=-1 -MATRIX=blosum62 - TRANS=human40.cdi -LIST=45
-DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100 - THR_MIN=0 - ALIGN=15 - MODE=LOCAL
-UOTFWM=Ppto -NORM=ext - HEAPSIZE=500 -MINLEN=0 - MAXLEN=200000000
-USER=US09976782_@CGN 1 1_64 @runat_31082004_115951_10328 -NCPD=6 - TCPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSEBLOCK=100 -LONGLOG
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSEBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -KGAPOP=10 -KGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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(c) 1993 - 2004 Compugen Ltd.
                                                         protein search, using frame_plus_n2p model
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C;Accession: S38744; A47472
R;Wisden, W.; Parker, E.M.; Mahle, C.D.; Grisel, D.A.; Nowak, H.P.; Yocca, F.D.; Felder, EsBS Lett. 333, 25-31, 1933
A;Title: Cloning and characterization of the rat 5-HT(5B) receptor. Evidence that the 5-13 A;Reference number: S38744; MUID:94039744; PMID:8224165
A;Recession: S38744; MUID:94039744; PMID:8224165
A;Recession: S38744; MUID:94039744; PMID:8224165
A;Recession: S38744; MUID:94039744; PMID:8224165
A;Recession: S4NA
A;Rederence number: Gards
A;Residues: 1-369 (MIS)
R;Elander, M.G.; Lovenberg, T.W.; Baron, B.W.; de Lecea, L.; Danielson, P.E.; Racke, M. R;Elander, M.G.; Lovenberg, T.W.; Baron, B.W.; de Lecea, L.; Danielson, P.E.; Racke, M. R;Elander, M.G.; Lovenbers of a distinct subfamily of 5-hydroxytryptamine receptors differenti A;Reference number: A47472; MUID:93234515; PMID:7682702
A;Reference number: A47472; MUID:93234515; PMID:7682702
A;Residues: 1-176, 'I', 'I77-369 (ERL)
A;Rosidues: 1-176, 'I', 'I77-369 (ERL)
A;Cross-references: GB:L10073; NID:9310074; PIDN:AAA40616.1; PID:9310075
A;Experimental source: hypothalamus
A;Note: sequence extracted from NCBI backbone (NCBIN:129665, NCBIP:129668)
C;Superfamily: octopamine receptor: transmembrane protein
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serotonin receptor 5B - rat N;Alternate names: 5-hydroxytryptamine receptor 5B (5-HTR5B) C;Species: Rattus norvegicus (Norway rat) C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999

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IGGAICCCCTICTICCTGACGGAACTCATCAGCCCACTTGTGCCTGCAGCCTGCCCCC 1021
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     CTAGTGCTGCTGATCGCTGCCACTTTCCTGTGGAACCTGCTGGTTCCGGTCACCATCCCG
                  LeuCysCysThrAlaSerIleTrpAsnValThrAlaileAlaLeuAspArgTyrTrpSer
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163 AlaLeuThrTrpAlaLeuSerAlaValIleSerLeuAlaProLeuLeuPheGlyTrpGly
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N;Alternate names: 5-hydroxytryptamine 5 receptor (5HTR-5)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_cl
C;Accession: S28058
R;Plassat, J.L.; Boschert, U.; Amlaiky, N.; Hen, R.
EMBO J. 11, 4779-4786, 1992
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I37107, Foord, S.; Goodson, S.; Bull, D.; Kilpatrick, G.; I FEBS Lett. 355, 242-246, 1994
A;Title: Cloning and characterisation of the human 5-HT5A serotonin receptor. A;Reference number: I37107; WUID:95080386; PMID:7988681
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|ThrAlaArgCysArgAlaThrValAlaPheGlnThrSerGlyAspSerTrpArgGluGln
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A.Molecule type: DNA
A.Residues: 1-357 <RES>
A.Cross-references: EMBL:X81411; NID:g541776; PIDN:CAA57168.1; PID:g784990
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A;Introns: 247/3
C;Superfamily: octopamine receptor type I
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                                                                                                     glycoprotein;
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Matches:
Conservative:
Mismatches:
Indels:
A,Title: The mouse 5HT5 receptor reveals a rem A,Reference number: $28058; MUID:93099851; PMI A,Accession: $28058
A,Accession: $28058
A,Status: preliminary
A,Wolecule type: DNA
A,Residues: 1-357 <PLA>
A,Cross-references: BMBL:Z18278
C,Superfamily: octopamine receptor type I
C,Keywords: G protein-coupled receptor: alv.com
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C.Species: Ratus norvegicus (Norway rat)
C.Species: Satus norvegicus (Norway rat)
C.Species: Satus norvegicus (Norway rat)
C.Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C.Accession: B47472
R.Erlander, M.G.; Lovenberg, T.W.; Baron, B.W.; de Lecea, L.; Danielson, P.E.; Racke, M. Proc. Natl. Acad. Sci. U.S.A. 90, 3452-3456, 1993
A;Title: Two members of a distinct subfamily of 5-hydroxytryptamine receptors differentian A;Title: Two members A47472; MUID:93234515; PMID:7682702
A;Reference number: A47472; MUID:93234515; PMID:7682702
A;Residues: preliminary
A;Nolecule type: nucleic acid
A;Residues: 1-357 < CRL>
A;Residues: 1-357 < CRL>
A;Residues: 1-357 < CRL>
A;Residues: SB:L10072; NID:9310072; PIDN:AAA40615.1; PID:9310073
A;Experimental source: hypochalamus
A;Experimental source: hypochalamus
A;Experimental source: type I
C;Superfamily: octopamine receptor type I
C;Keywords: G protein-coupled receptor; transmembrane protein
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278 GlnLysGluGlnArgAlaAlaLeuMetValGlyIleLeulleGlyValPheValLeuCys
                                                                                                                                                                                           318 IleTrpLysSerIlePheLeuTrpLeuGlyTyrSerAsnSerPhePheAsnProLeuIle
                                                                                                                                                                                                                                                                                                                                                     TACACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAGA
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                                                                     CAGAAGGAGGCGAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTGT
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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5-hydroxytryptamine 5 alpha receptor - rat
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60.85%
47.10%
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127

110

||| |||||||| LeuvalMetProLeuSerLeuvalHisGluLeuSer---GlyArgArgTrpGlnLeuGly 111

92

CGGAGCCTGTGCCACGTGTGGATCTCCTTCGACGCCGGAGCCTGTGTGCTGCCCCGCC

į	-09-976-782-15 (1-1152	Qy 167 GTCCTGGTGGTGCTGCTAGTGCTGCTGATGCTGCCACTTTCCTGTGGAACCTGCTG 226	227 GTTCCGGTCACCATCCCGCGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCC	ValValAlaThrValTyrArgThrArgLysLeuHisThrProAlaAsnTyrLeulleAla 88 TCGACGGCCGTCTCGGACGAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGT 34	347	407 TTCGACGCGGAGCCTGTCTGTGCTCCCCGCGCCTCGGGAACGGCCGCCATCGCC 46	Oy 467 CTGGGCCGACGGGGCCATCACGCGCCTGCGGCACCTGCGCACCCGCACCCGCACCGC 526			Oy 647 GAACCCTCCTATGCCGCCTTCTCCACCGGGGGGCTTCCACCTGCGCTTGGCGTG 703 1::	Qy 704 GTGCCGTTTGTCTACCGGAAGATCTACGAGGCCGAAGTTTCGTTTC 751 :::	Oy 752CGGCGCCGCCGGAGAGCTGTGCTG	Qy 779 TIGCCGGCCACCAIGCAGGIGAGGICCAAGGIAAGGAAGCACCIGAIGAGGCIGAA 835 :: :: ::	836 GIGGIGITCACGCACATIGCAAGCAACGGIGICCTICCAGGIGAGCGGGGACTCCTGG	Db 283 ProValTyrValAsnGlnValLysValArgValSerAspAlaLeu 297 Ov 896 CGGGAGCAGCAAG	298 LeuGluLysLysLeuMetAlaAlaArgGluArgLysAlaThrLysThrLeuGlylle 31	QY 938 CTGATTGGCGTGTTTGTGCTGGATCCCCTTCTTCCTGACGGAACTCATCAGCCCA 997	998 CTCTGTGCCTGCAGCCTGCCCCCATCTGGAAAAGCATATTTCTGTGGCTTGGC	DD 338 ILECYSLYSEASPALACYSTIPPHEHISGINALAILEPHEASPPHEFNETNTTFPLEUGLY 357 QY 1052 TACTCCAATTCTTCAACCCCCTGATTTACACACACTTTTAACAAGAAGCTACAAACAA	358 TyrValAsnSerLeuIleAsnProllelleTyrThrMetSerAsnGluAspPheLysGln 377	Qy 1112 GCCTTCAAGAGCCTC 1126
440 GGCCTCGGGAACGTGGCGGCCATCATCACCTGGGCCACCATCATCATCACGAACGTGACACCACAACAACGAACAACAACAACAACAACAACAACA	SerileTrpAsnValThrAla1leAlaLeuAspArgTyrTrpSerileThrArgHisLeu 14	500 CAGCACGCTGCGCACCCGCAGCCGCGCCTTGCTTGATCGCGCTCGCCCGGGTG 559 :::::	CCGTCGGCGCTCATCGCCCTCGCGCCGCTCTTTGGCCGGGGCGAGGTGTGCGACGCT	168 LeuserAlavallieSerLeuAlaProLeuLeuPneGlyTrpGlyGluThrTyrSerGlu 187 620 CGGCTCCAGCGTGCCAGGTGAGCCGGGAACCCTCCTATGCCGCCTTCTCCACCGGGGC 679 188 LanserGlyGlyGlyGlyGlGaalavaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG	GCCTTCCACCTGCCGCTTGGCGTGCGCTTTGTCTACCGGAAGATCTACGAGGCGGCC		797 GTGAGGTCCAAGGTAAAGGAAGCACCTGATGAGGCTGAAGTGGTGTTCACGGCACATTGC 856 248VallysAspalaSerGlnHisProGlnMetValPheThrValArg 262	857 AAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGGGAGCAGAGGAGGCGA 916	917 GCAGCCATGATGGTGGAAATTCTGATTGGGGTGTTTGTGCTGTGCTGGATCCCCTTCTTC 976 283 AlaAlaLeuMetValGlyIleLeuIleGlyValPheValLeuCysTrpPheProPhePhe 302	977 CTGACGGAACTCATCAGCCCACTCTGTGCCTGCAGCCCCCCCATCTGGAAAAGCATA 1036 :::	1037 ITICIGIGGCITGGCIACTCCAATTCTTCAACCCCCTGATTACACAGCTTTTAAC 1096 	1097 AAGAACTACAAAGCCTTCAAGAGCCTCTTTACTAAGCAGAGA 1141 :::::: :::::	in receptor 1D beta - rabbit	and animals. 2-lyvinoxy/irpuramille receptor in pera (3-miximbera) is: Oryctolagus cuniculus (domestic rabbit) i5-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999	lon: S6642.2 d, G.; Lockyer, M.; Giles, H.; Fairweather, N. t. 377, 73-76, 1995	Cloning and characterisation of the rabbit 5-HT(1D-alpha) and 5-HT(1D-beta) rection under: S68422; MUID:96130324; PMID:8543023		reterences: EMBL:230163; NID:91004283; PIDN:CAA90531.1; PID:91004284 amily: vertebrate rhodopsin ds: neurotransmitter receptor	2 Length:	Score: 449.00 Matches: 118 Percent Similarity: 51.59% Conservative: 60	34.20% Mismatches: 20.84% Indels:

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Cikeywords: G protein-coupled receptor; glycoprotein; lipoprotein; neurotransmitter rece
F;50-75/Domain: transmembrane #status predicted <TM1>
F;84-112/Domain: transmembrane #status predicted <TM2>
F;124-145/Domain: transmembrane #status predicted <TM3>
F;124-15/Domain: transmembrane #status predicted <TM3>
F;206-229/Domain: transmembrane #status predicted <TM3>
F;206-229/Domain: transmembrane #status predicted <TM3>
F;21-33/Domain: transmembrane #status predicted <TM6>
F;24,32/Binding site: carbohydrate (Ann) (covalent) #status predicted
F;25-313/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict
F;25-313/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predict
F;388/Binding site: palmitate (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCTTCCACCTGCCGCTTGGCGTGGTGCCGTTTGTCTACGGAAGATCTACGAGGCGGCC 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 GCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGACGTCGGCTGCTGGGCCGG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 CGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTCTCGGACGAACTAGTGGCAGCGCTG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 ValValCysAspPheTrpLeuSerSerAsp-----IleThrCysCysThrAlaSer 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 GGGCCGCCCTTCTCTGTCTTCACGGTCCTGGTGACGCTGCTAGTGCTGCTGATCGCT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCGAGACCAGCAGCGGACCCCGAAGCCCCGAGAGGGATACTCGGTTCGACCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 GCCACTITCCTGTGGAACCTGCTTCCGGTCACCATCCCGCGGGTCCGTGCCTTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 CICGGGAACGIGGCGGCCAICGCCCIGGGCCGCGACGGGCCAICACACGCCACCTGCAG
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Mismatches:
Indels:
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A,Map position: 6q14.3-6q16.3
C,Superfamily: vertebrate rhodopsin
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32.32%
20.80%
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A;Recension: MAINE A2146, MUDD:92210926; FMID:1348246
A;Recension: MAINE A2146
A;Recension: MAINE BANK A;R. MILLER, K.; Teitler, M.; Hoffman, B.J.; Kennedy, J.L.;
Proc. Natl. Acad. Sci. U.S. A. 89, 5522-5526, 1992
A;Ritler A human serotonin 1D receptor variant (strubbea) encoded by an intronless gene A;Reference number: A45261, MUD:9230275; FMID:1351684
A;McCession: A45261
A;McCessreferences: GB:M73128; NID:9184459; PIDN:AAAS8675.1; PID:9184460
A;Reference number: A45261, MUD:9230275; PMID:1351684
A;McCessreferences: GB:M73128; NID:9184459; PIDN:AAAS8675.1; PID:9184460
A;References: GB:M73128; NID:9184459; PIDN:AAAS8675.1; PID:9184464
A;References: GB:M73128; NID:9184459; PIDN:AAAS8675.1; PID:9184464
A;Reference number: A44309, MUD:92218412; PMID:1559993
A;Richer Lobercoller Comming of a human serotonin receptor (812) with a pharmacological proposed communer: A44309, MUD:92218412; PMID:1559993
A;Reference number: A44309, MUD:92218412; PMID:1559993
A;Rote: authors proposed that this is the 5-AptroxytryPramine ID subtype receptor Proc. Natl. Acad. Sci. U.S.A. 89, 3330-3534, 1992
A;Rote: authors proposed that this is the 5-AptroxytryPramine ID subtype receptor Proc. Natl. Acad. Sci. U.S.A. 89, 3330-3534, 1992
A;Rote: authors proposed that this is the 5-AptroxytryPramine ID subtype receptor Proc. Natl. Acad. Sci. U.S.A. 89, 3330-3534, 1992
A;Rote: authors proposed that this is the 5-AptroxytryPtamine ID subtype receptor Proc. Natl. Acad. Sci. U.S.A. 89, 3330-3534, 1992
A;Rote: authors proposed that this is the 5-AptroxytryPtamine ID subtype acceptor is encoded by a subfamily of two distinct genes: 5-Aptrossion: B49844
A;Rote: authors proposed that this is the 5-AptroxytryPtamine ID subtype acceptor is the subtype acceptor is encoded by a subfamily of two distinct genes: 5-AptroxytryPtamine ID subtype acceptor is the subtype acceptor is encoded by a subfamily of two distinct genes: 5-AptroxytryPtamine ID subtype acceptor is the subtype acceptor is the 
                                                                                                                                                                                                               N; Alternate names: 5-hydroxytryptamine 1D receptor beta; 5-hydroxytryptamine receptor 1B (Alternate names: 5-hydroxytryptamine 1D receptor beta; 5-hydroxytryptamine receptor 1B (Species: Homo sapiens (Man) (C; Species: Homo sapiens (Man) (Mostalia) (Mostalia)
                                                                                                                                                                                        serotonin receptor 1B - human
N'Alternate names: 5-hydroxytryptamine 1D receptor beta; 5-hydroxytryptamine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Jin, H.; Oksenberg, D.; Ashkenazi, A.; Peroutka, S.J.; Duncan, A.M.V.; Rozmahel, J. Biol. Chem. 267, 5735-5738, 1992
A; Title: Characterization of the human 5-hydroxytryptamine-1B receptor.
A; Reference number: A42146; MUID:92210526; PMID:1348246
                               AlaPheHisLysLeu 382
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	Oy 587 CTGCTCTTTGGCGGGGCGGAGGTGTGGGCTCCAGGGCTGCCAGGTGAGCCGG 646 185PhePheTrpArgGlnAlaLysAlaGluGluGluValSerGluCysLeuValAsnThr 203 Qy 647 GAACCCTCTATGCCGCTTCTCCACCGGGGCCTTCCACTGCGGTTGGGGTG 703 1::		RESULT 9 B30341 G protein-coupled receptor RDC4 - dog C protein-coupled receptor RDC4 - dog C protein-coupled receptor RDC4 - dog C protein-coupled Sequence revision 07-Jun-1990 #text_change 05-Nov-1999 C; Accession: B30341; S12822 R; Libert, F:; Parmentier, M.; Lefort, A.; Dinsart, C.; Van Sande, J.; Maenhaut, C.; Simon Science 244, 569-572, 1989 A; Title: Selective amplification and cloning of four new members of the G protein-couplec A; Reference number: A30341; MUID:89242119; PMID:2541503 A; Accession: B30341 A; Status: nucleic acid sequence not shown A; Molecule type: mRNA A; Residues: 1-377 < LIB>
Qy 740 AAGTTTCGTTTC	CGAGCAGCCATGATGGCGTGTTTGTGTGTGTGTGTGTGTG	RESULT 8 S58126 Scores: Notice and the complete of Secretarian receptor 1-like - rabbit Notice and the secretarian receptor 1-like (5-HTR) C; Species: Oryctolagus cuniculus (domestic rabbit) C; Accession: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999 C; Accession: S58126 R; Wurch, T.; Cathala, C.; Palmer, C.; Valentin, J.P.; John, G.; Colpaert, F.C.; Pauwels, Submitted to the EMBL Data Library, July 1995 A; Reference number: S58126 A; Reference number: No.: No.: No.: No.: No.: No.: No.: No.	Oy 167 GTCCTGGTGGTGGTGGTGGTGGTGGTGGTGCTGCCACTTTCCTGTGGAACCTGCTG 226

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Serotonin receptor 1B - Chinese hamster
NyAlternate names: 5-hydroxytryptamine receptor 1B (5-HTR1B)
(;Species: Cricetulus griseus (Chinese hamster)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C;Accession: 554133
R;Wurch, T.; Palmier, C.; Colpaert, F.C.; Pauwels, P.J.
R;Wurch, T.; Palmier, C.; Colpaert, F.C.; Pauwels, P.J.
A;Reference number: 554153
A;Accession: 854153
A;Accession: 854153
A;Accession: S41153
A;Residues: 1-386 < WURA
A;Molecule type: mRNA
A;Residues: 1-386 < WURA
A;Residues: 1-386 < WURA
A;Cross-references: EMBL:X86458; NID:g790985; PIDN:CAA60175.1; PID:g790986
C;Superfamily: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor
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                                                220 ilelyrvalAlaAlaArgAsnArgIleLeuAsnProProSerLeuTyrdlyLysArgPhe
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A;Cross-references: EMBL:X14049; NID:g900; PIDN:CAA32207.1; PID:g901
R;Libert, F.; Parmentier, M.; Lefort, A.; Dumont, J.E.; Vassart, G.
Nucleic Acids Res. 18, 1916, 1990
A;Title: Complete nucleotide sequence of a putative G protein coupled B;Reference number: S12822; MUID:90245610; PMID:2159630
A;Accession: S12822
A;Status: translation not shown
A;Molecule type: MINA
A;Molecule type: MINA
A;Residues: 1-377 <LI2>
A;Cross-references: EMBL:X14049; NID:g900; PIDN:CAA32207.1; PID:g901
C;Genetics:
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C,Superfamily: octopamine receptor type
C,Keywords: G protein-coupled receptor;
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A;Status: preliminary
A;Molecule type: DNA
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NyAlternate names: 5-hydroxytryptamine 1B receptor (5HTR-1B)
Systemate names: 5-hydroxytryptamine 1B receptor (5HTR-1B)
Systemate names: 5-hydroxytryptamine 1C; Species: Mar.1993 (buse mouse)
C;Date: 04-Mar.1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A42688; S22191
E;Maroteaux, 1.; Saudou, F.; Analaky, N.; Boschert, U.; Plassat, J.L.; Hen, R.
Proc. Natl. Acad. Sci. U.S.A. 89, 3020-3024, 1992
A;Title: Mouse 5HT1B serotonin receptor: cloning, functional expression, and localizatic A;Accession: A42688; MUID:92212959; PMID:1557407
A;Status: preliminary
                                                                                                                       CICTGI-----GCCIGCAGCCIGCCCCCCAICIGGAAAAGCAIAIITCIGIGGCTIGGC 1051
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               GCCTCGTTGCTCATGATCGCGCTCGCCCGGGTGCCGTCGGCGCTCATCGCCCTCGCGCCC
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AspHisValLeuTyrThrValTyrSerThrGlyGlyAlaPheTyrLeuProThrLeuLeu
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                                                   TTCGACGCCGGAGCCTGTCTGTGCTGCCCCGCCGGCCTCGGGAACGTGGCGGCCATCGCC
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C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmen
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|LeuValMetPro-----lleSerThrMetTyrThrValThrGlyArgTrpThrLeuGly
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A;Molecule type: DNA
A;Residues: 1-386 cAMR>
A;Residues: 1-386 cAMRA
A;Cross-references: GB:M85151; NID:g191529; PIDN:AAA83221.1; PID:g191530
A;Note: sequence extracted from NCBI backbone (NCBIN:93807, NCBIP:93808)
A;Note: sequence extracted from NCBI backbone (NCBIN:93807, NCBIP:93808)
B;Saudou, F.
Submitted to the EMBL Data Library, January 1992
A;Reference number: S22191
                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:211597; NID:g49756; PIDN:CAA77678.1; PID:g49757
C;Superfamily: vertebrate rhodopsin
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Conservative:
Mismatches:
Indels:
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438.00
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20.33%
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Oy 227 GTTCCGGTCATCCCGCGGGTCCTTCCACCGCGTGCCGTAACTTGGTGGCC 286	407 Trogacogacorgrands	Db 141 LeuAspArgfyrTrpAlailefhrAspAlaValAspfyrSerAlaLysArginrFroLys 160 Qy 527 GCCTCGTTGCTCATGATCGCGCTCGCCGGGTGCCGTCGGCGTCATCGCCCTCGCGCCG 586 161 ArgAlaAlaileMetileValruValTrpValpheSerIleSerIleSerLeuProPro 180 Qy 587 CTGCTCTTTGGCCGGGGGGGGGGGGGCTCCGGCTCCAGGGTGGCCGG 646	647 GAACCCTCCTATGCCGCCTTCTCCCCGCGCCTTCCTCCGCCTTGGCGTG 70 .:: ::	704 GTGCCGTTTGTCTACCGGAGGTCTACGAGGCGGCCAAGTTTCGTTTC	260	Oy 836 GTGGTTCACGGCACATTGCAAGCAACGTGTCCTTCAGGTGACGGGGACTCTGG 875 Db 280 ProValTyrValAsnGlnValLysValArgValSerAspAlaLeu 294 Oy 896 CGGGAGCAGAGGAGAGCGAGCAGCCATGATGGTGGAATT 937 Db 295 LeuGluLysLysLysLeumetAlaAlaArgGluArgLysAlaTnrLysThrLeuGlyIle 314	OY 938 CTGATTGGCGTGTTTGTGCTGGATCCCCTTCTTCCTGACGGAACTCATCAGCCCA 997. 315 IleLeuGlyAlaPheIleValCySTTpLeuProPhePheIlelSerLeuValMetPro 334 Qy 998 CTCTGTGCCTGCAGCCTGCCCCCATCTGGAAAAGCATATTCTGTGGTTGGCTTGGC 1051 335 IleCysLysAspAblaCySTTpPheHisMetAlaIlePheAspPhePheAsnTTpCtGTGJY 354	1052 355 1112 375	RESULT 13 A38271 serotonin receptor 7 - fruit fly (Drosophila melanogaster) N;Alternate names: 5-hydroxytryptamine receptor 7 (5-HTR7)
Qy 737 GCCAAGTTTCGTTTC	Qy 869 TCCTTCCAGGTGAGCGGGAGCAGAAGGAG 910	QY 971 TTCTTCCTGACGGAACTCATCAGCCCACTCTGTGCCTGCAGCCTGCCCCCATC 1024 ::: :::	Oy 1085 ACAGCTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTC 1126	RESULT 12 \$18637 serotonin receptor 1B - rat NyAlternate names: 5-hydroxytryptamine receptor 1B (5-HTR1B) C;Species: Rattus norvegicus (Norway rat) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 C;Accession: \$18637; 157683 B;Voice M	EMBO J. 10, 4017-4023, 1991 A,Title: Molecular cloning and characterization of a rat brain cDNA encoding a 5-hydroxy a,Reference number: \$18637; MUID:92097519; PMID:1836757 A,Accession: \$18637 A,Status: preliminary	A;Molecule type: mRNA A;Residues: 1-386 <voi> A;Cross-references: EMBL:X62944; NID:g57509; PIDN:CAA44716.1; PID:g57510 A;Cross-references: EMBL:X62944; NID:g57509; PIDN:CAA44716.1; PID:g57510 R;Hamblin, M.W.; McGuffin, R.W.; Metcalf, M.A.; Dorsa, D.M.; Merchant, K.M. Mol. Cell. Neurosci. 3, 578-587, 1992 A;Title: Distinct 5-HT1B and 5-HT1D serotonin receptors in rat: structural and pharmacol A;Reference number: I57683</voi>	A;Accession: 157683 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-386 <res a;crose-references:="" c;keywords:="" c;superfamily:="" g="" gb:m89594;="" nid:g202542;="" pid:g202543="" pidn:aaa40613.1;="" protein-coupled="" protein<="" receptor;="" rhodopsin="" ss="" td="" transmembrane="" vertebrate=""><td>Scores: 3.11e-21 437.00 imilarity: 51.01% 1 Similarity: 20.29% ch:</td><td>US-09-976-782-15 (1-1152) x S18637 (1-386) QY</td></res>	Scores: 3.11e-21 437.00 imilarity: 51.01% 1 Similarity: 20.29% ch:	US-09-976-782-15 (1-1152) x S18637 (1-386) QY

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serotonin receptor 5-HT precursor - Caenorhabditis elegans
C'Species: Caenorhabditis elegans
C'Species: Caenorhabditis elegans
C'Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C'Accession: T42203
R'Olde, B.; McCombie, W.R.
J. MOL, Neurosci. 8, 53-62, 1997
J. Mol. Neurosci. 8, 53-62, 1997
A;Ritle: Molecular cloning and functional expression of a serotonin receptor from Caenorh
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|LeuLeulleLeuGlyAsnGluHisGluAspGluGluGlyGlnProlleCysThrValCys 317
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LysLysAlaSerThrThrLeuGlyIleIleMetSerAlaPheThrValCysTrpLeuPro
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MetLeuPheValTyrTyrGInIlePheArgAlaAla-------
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Matches:
Conservative:
Mismatches:
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1.445 < CUL)
A,Cross-references: EMBL:U15167; PIDN:AAB66360.1
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                                                     R;Witz, P.; Amlaiky, N.; Plassat, J.L.; Maroteaux, L.; Borrelli, E.; Hen, R. Proc. Natl. Acad. Sci. U.S.A. 87, 8940-8944, 1990
A;Title: Cloning and characterization of a Drosophila serotonin receptor that activates A;Reference number: A38271; MUID:91062395; PMID:2174167
                                                                                                                                                                                                                                                A,Gene: FlyBase:5-HT7
A,Cross-references: FlyBase:FBgn0004573
C;Superfamily: octopamine receptor type I
C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein; phosphoprotein
                                                                                                                                                                                                                  residue
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                                                                                                                                                                                                                  for
C;Species: Drosophila melanogaster
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 04-Sep-1998
C;Accession: A38271 Rsequence_revision 7.1.; Maroteaux, L.; Borrelli, E.; Hen, R.
R;Witz, P.; Amlaiky, N.; Plassat, J.L.; Maroteaux, L.; Borrelli, E.; Hen, R.
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A;Cross-references: GB:M5533
A;Note: the authors translated the
C;Genetics:
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A, Map posttion: 1p36.3-1p34.3
A, Introns: #status absent ceceptor type I
C, Superfamily: octopamine receptor type I
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A, Molecule type: mRNA
A, Residues: 1-377 <WEI>
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                                                                                                22 SerAlaValAlaArgGlyThrHisLeuValAspGlnPheProAlaHisAlaGluIlePhe
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                        CTTGCCCTGGGACCCGAGACCAGCGGACCCGGGACCCCAAGCCCGAGAGGGGATACTC
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                                                LeuAsnLeuThrAlaSerProSerSerGlnProAlaThr-
US-09-976-782-15 (1-1152) x T42203 (1-445)
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serotonin receptor 1D - human
NiAlternate names: 5-hydroxytryptamine receptor 1D (5-HTR1D); 5HT-1D alpha receptor
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A53279; A44136
R;Hamblin, M.W.; Metcalf, M.A.
Mol. Pharmacol. 40; 143-148; 1991
A;Pitle: Primary structure and functional characterization of a human 5-HT-1D-type serot
A;Reference number: A53279; MUD:91342595; PMID:1652050
A;Residues: 1-377 < HAM*
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R;Weinshank, R.L.; Zgombick, J.M.; Macchi, M.J.; Branchek, T.A.; Hartig, P.R.
Proc. Natl. Acad. Sci. US.A. 89, 3630-3634, 1995
A;Title: Human serotonin 1D receptor is encoded by a subfamily of two distinct genes: 5-A;Reference number: A44136; MUID:92228840; PMID:1565658
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C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416 LeuasnProllelleTyrThrValPheSerGlnAspPheArgAlaAlaPheLysArg1le 435
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336 IleAspGluGluAsnGlyArgSerLysProGlyIleValLysArgArgArgArgThrLys 355
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                                                                                                       376 ThrPheValAlaCysTrpThrProPhePheLeuValSerIleTyrArgProIleCysGly
                                                                                                                                                                                                                                                                                                                                                                                 947 GIGITTIGIGCIGIGCIGGAICCCCTICTICTICTGACGGAACICAICAGCCCACTCTGIGCC
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                                                                   887 GACTCCTGGCGGGAGCAGAAGGAGAGGCGAGCAGCATGATGATGGTGGGAATTCTGATTGGC
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C; Genetics:
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287 GluArgLysArgIleSerAlaAlaArgGluArgLysAlaThrLysIleLeuGlyIleIle 306
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                                                      224 CTGGTTCCGGTCACCATCCCGCGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTG 283
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   ---AlaThrValLeuSerAsnAla
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Sequence 16, Application US/09976782

Publication No. US20030190715A1

GENERAL INFORMATION:

APPLICANT: Grosse et al

TITLE OF INVENTION: No. US20030190715A1e1 Proteins and Nucleic Acids Encoding Same

FILE REPERENCE: 21402-157

CURRENT APPLICATION NUMBER: US/09/976,782

CURRENT PILING DATE: 2001-10-12

PRIOR PELICATION NUMBER: 60/240,113

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PRIOR PILING DATE: 2000-10-16

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PRIOR APPLICATION NUMBER: 60/240,733

PRIOR PILING DATE: 2000-10-16

PRIOR PILING DATE: 2000-10-16
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSTZE=500 -MINLEN=0
-MAXTEN=200000000 - USER=US09976782 @CGN 1 1 225 @runat 31082004 115953 10443
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                            August 31, 2004, 20:21:44 ; Search time 160 Seconds (without alignments) 4530.426 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                OM nucleic - protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                    1297172 segs, 314612898 residues
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Match Length DB
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D
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Database

Result No.

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US-10-333-946-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B. APPLICANT: ARVIZU, Chandra S.; LAL, Preeti G. APPLICANT: BURFORD, Neil; YUE, Henry APPLICANT: BURFORD, Neil; YUE, Henry APPLICANT: RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R., APPLICANT: KALLICK, Deborah A.; GHRMLA, Nariah R., APPLICANT: KALLICK, Deborah A.; GHRMLA, Nariah R., APPLICANT: LU, Yan; TRIBOULEY, Catherine M. APPLICANT: POLICKY, Jennifer L.; KEARNEY, Liam, APPLICANT: GRAUL, Richard C.; WARREN, Bridget A.; APPLICANT: GRAUL, Richard C.; WARREN, Bridget A.; APPLICANT: LEE, Ernestine A.; DING, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: G-FKOLDEIN COULDED ADDRESS.
FILE REFERENCE: PI-0176 USN
CURRENT APPLICATION NUMBER: US/10/33,946
CURRENT FILING DATE: 2003-01-22
PRIOR PELING DATE: 2001-07-25
PRIOR PLING DATE: 2001-07-27
PRIOR PLING DATE: 2000-07-27
PRIOR PLING DATE: 2000-08-03
PRIOR PLING DATE: 2000-08-03
PRIOR PLING DATE: 2000-08-03
PRIOR PLING DATE: 2000-08-03
PRIOR PLING DATE: 2000-08-14
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US-10-333-946-15
Sequence 15, Application US/10333946
Publication No. US20040023252A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/240,669
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/262,455
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2000-10-16
PRIOR FILING DATE: 2000-10-16
NUMBER OF SEQ ID NOS: 127
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 379
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CRGANISM: Homo sapiens
US-09-976-782-16
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Db 292 LysGluArgArgAlaAlaMetWetValGlyIleLeuIleGlyValPheValLeuCysTrp 311 Qy 965 ATCCCTTCTTGACGAACTCATCAGCCCATCTGTGCCTGCAGCTGCCCCCATC 1024	Qy 1085 ACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGAGA 1141	RESULT 3 US-09-823-187-10 ; Sequence 10, Application US/09823187 ; Publication No. US20030096952A1	; GENERAL INFORMATION: ; APPLICANT: Burgess, Catherine ; APPLICANT: Gusev, Vladimir X ; APPLICANT: Liu, Xiaohong	; APPLICANT: Majumder, Kumud ; APPLICANT: Padigaru, Muralidhar ; APPLICANT: Patturajan, Meera ; APPLICANT: Shimkets, Richard A	; APPLICANT: Spaderna, Steven K ; APPLICANT: Spytek, Kämberly ; APPLICANT: Taupier, Raymond J ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME	; FILE REFERENCE: 15966-745 ; CURRENT APPLICATION WUMBER: US/09/823,187 ; CURRENT FILING DATE: 2001-03-29 ; PRIOR APPLICATION NUMBER: 60/193,339	; PRIOR FILING DATE: 2000-03-30 ; PRIOR APPLICATION UNMBER: 60(193,205 ; PRIOR FILING DATE: 2000-03-30 ; PRIOR APPLICATION NUMBER: 60/195,343		; PRIOR FILING DATE: 2000-04-06 ; PRIOR APPLICATION VUMBER: 60/195,792 ; PRIOR FILING DATE: 2000-04-10 ; PRIOR APPLICATION NUMBER: 60/196,556	; PRIOR FILING DATE: 2000-04-11 ; PRIOR APPLICATION NUMBER: 60/197,081 ; PRIOR FILING DATE: 2000-04-13 ; PRIOR APPLICATION NUMBER: 60/197,525	; PRIOR FILING DATE: 2000-04-14 ; PRIOR APPLICATION NUMBER: 60/197,087 ; PRIOR FILING DATE: 2000-04-14 ; NUMBER OF SEQ ID NOS: 103	; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 10 ; LENGTH: 370 ; TYPE: PRT	ORGANISM: Homo sapi. 9-823-187-10 nment Scores:	2.26e-107 1860.50 larity: 97.63% imilarity: 97.63%	Indels: Gaps: 823-187-10 (1-370)	Oy S ATGAGGCCGCTAGCCTTTCAGTGCCCACCGCCGCGTTGCCCTTGCCCTGGGACCCGAG 64
Alignment Scores: Pred. No.: Rocate: Score: Score: 1.96e-107 Matches: 370 Matches: 97.63\$ Mismatches: 0 Query Match: 16 Gaps: 16 Gaps: 3 US-09-976-782-15 (1-1152) x US-10-333-946-15 (1-370)	Qy 5 ATGGAGGCCGCTATCAGTGGCCACCGCGGGGTTGCCCTTGCCCTGGGACCGGG 64	Oy 65 ACCAGGACCCGAGACCCCAAGCCGAGAGGATACTCGGTTCGACCCCGAGGGC 124 Db 21 ThrSerSerGlyThrProSerFroArgGlyIleLeuGlySerThrProSerGly 38	Oy 125 GCCGTCCTGCCGGCCGAGGCCGCCCTTCTCTGTCTTCACGGTCCTGGTGACGCTG 184	Qy 185 CTAGTGCTGATCGCTGCACTTTCCTGTGGAACCTGCTGGTTCGGGTCACCATCCCG 244	Qy 245 CGGGTCCGTGCCTTCCACCGCGTGCCGACGACGGCCTCGACGGCCGTCTCGGAC 304 Db 79 ArgValArgAlaPheHiSArgValProHisAsnLeuValAlaSerThrAlaValSerAsp 98	Oy 305 GAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGA 364	Qy 365 CGTCGGCTGGCCGGAGCCTGTGCCACGTGGATCTCCTTCGACGCGGAGCCTGT 424 Db 119 ArgArgLeuLeuGlyArgSerLeuCysHisValIrplIeSerPheAspAla 135	Oy 425 CIGIGCTGCCCGCGGCCTCGGGAACGIGGCGGCCATCGCCCTGGGCCGCGACGGGCC 484	OY 485 ATCACACGCACCTGCAGCACACGCGCGCCCCCGCGCCCCCGCGCTCGTTGCTC 544	OY 545 GCGCTCGCCCGGTCGCCGTCATCGCCCTCGCGCCGCTGCTCTTTGGCCGGGGC 604	OY 605 GAGGTGTGCGACGCTCCAGCGCTGCCAGGTGAGCGGGAACCCTCCTATGCCGCC 664	Qy 665 TICTCCACCGGGGGCCTTCCACCTGCCGCTGGGGGGGGGCGTTTGTCTACCGGAAG 724	QY 725 ATCTACGAGGCGCCAAGTTTCGTTTCGGCCGCCGCGGAGAGCTGTGCTGCCGTTGCCG 784 DD 236 IleTyrGluAlaAlaLysPheArgPheGlyArgArgArgArgArgAlaValLeuProLeuPro 255	Oy 785 GCCACCAIGCAGGIGAGGICCAAGGIAAAGGAACCACCIGAIGAGGCIGAAGIGGIGIIC 844	Oy 845 ACGGCACATTGCAAAGGAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGGGGGGGG	Oy 905 AAGGAGGCGAGCCATGATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTGG 964

MetGluAlaAlaSerLeuSerValAlaThrAlaGlyValAlaLeuAlaLeuGlyProGlu

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APPLICANT: Burgess, Vladimir Y
APPLICANT: Gusev, Vladimir Y
APPLICANT: Gusev, Vladimir Y
APPLICANT: Majunder, Kundd
APPLICANT: Padigaru, Muralidhar
APPLICANT: Padigaru, Muralidhar
APPLICANT: Spaderna, Steven K
APPLICANT: Laupier, Raymond J
TITLE OF INVENTION: NOVEE PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: 15966-745
CURRENT APPLICATION NUMBER: 60/193,339
PRIOR PRILING DATE: 2000-03-30
PRIOR PRILING DATE: 2000-04-05
PRIOR PRILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR PRILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-10
PRIOR PLILING DATE: 2000-04-10
PRIOR PLILING DATE: 2000-04-11
PRIOR PLILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Patentin Ver: 2.1
FENDING DATE: 2000-04-14
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             ; Sequence 12, Application US/09823187; Publication No. US20030096952A1
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ORGANISM: Homo sapiens
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                          1 ThrSerSer-----GlyThrProSerProArgGlyIleLeuGlySerThrProSerGly
                                                                                                         39 AlaValLeuProGlyArgGlyProProPheSerValPheThrValLeuValValThrLeu
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ACCAGCAGCGGACCCCGAAGCCCGAGAGGGATACTCGGTTCGACCCCGAGCGG
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APPLICANT: MACHAEL MARK L.
APPLICANT: THORNTON, MACHAEL B.
APPLICANT: THORNTON, MACHAEL B.
APPLICANT: THORNTON, MACHAEL B.
TILLE G. INVENTION: G-PROTEIN COUPLED RECEPTORS FILE REFERENCE: PI-0131 USN
CURRENT APPLICATION NUMBER: US/10/311,671
CURRENT APPLICATION NUMBER: DCI/19275
PRIOR APPLICATION NUMBER: PCT/US01/19275
PRIOR APPLICATION NUMBER: 60/212,483
PRIOR FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/212,209
PRIOR PELING DATE: 2000-06-22
PRIOR PELING DATE: 2000-06-22
PRIOR PLING DATE: 2000-06-29
PRIOR FILING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PLILING DATE: 2000-07-07
PRIOR PLILING DATE: 2000-07-07
PRIOR PLILING DATE: 2000-07-14
PRIOR PLILING DATE: 2000-07-14
PRIOR PLILING DATE: 2000-07-21
PRIOR PLILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PERL PROGRAM
SEQ ID NO 8
LENGTH: 372
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NAME/KEY: misc_feature
OTHER INFORMATION: 1ncyte ID No: 7474977CD1
                                              LU, Dyung Aina M.
TRIBOULEY, Catherine
                                                                                                                                                       ELLIOTT, VICKI S.
HERNANDEZ, Roberto
WALSH, Roderick T.
BOROWSKY, Mark L.
THORNTON, Michael B.
                                                                                                                   YANG, Junming
RAMKUMAR, Jayalaxmi
AU-YOUNG, Janice K.
ELLIOTT, Vicki S.
                                                                     LU, Yan
CHAWLA, Narinder K.
GRAUL, Richard
YAO, Monique G.
                       KHAN, Farrah A.
ARVIZU, Chandra S.
GRIFFIN, Jennifer
           YUE, Henry
KHAN, Farra
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ORGANISM: Homo sapiens
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                                                                 CTGTGCTGCCCCGCCGGGCCTCGGGAACGTGGCGGCCATCGCCCTGGGCCGCGACGGGGCC
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Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                        US-09-976-782-15 (1-1152) x US-10-311-671-8 (1-372)
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Sequence 8, Application US/10311671 Publication No. US20040072996A1 GENERAL INFORMATION:

US-10-311-671-8

APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: LAL, Preeti G.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: HAFALIA, April J. A.
APPLICANT: GANDHI, Ameena R.
APPLICANT: KALLICK, Deborah A.

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GORMAN, LINDA
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APPLICANT: SHENOVACK, UNITED FOR APPLICANT: SHENOY, SHERE IS APPLICANT: SHITHSON, CHERKE IS APPLICANT: SHITHSON, CHERKE IS APPLICANT: SHITHSON, CHERKE IS APPLICANT: STRENGER, DAVID
APPLICANT: STRENGER, SHENER FOR APPLICANT: STRENGER, DAVID
APPLICANT: STRENGER, SHENER FOR APPLICANT: STRENGER, DAVID
APPLICANT: STRENGER, SHENER FOR APPLICANT: SOUTH SHENER FOR APPLICANT: SOUTH SHENER FOR APPLICANT: SOUTH SHENER FOR APPLICANT: NUMBER: 60/233,382
FILTE REFERENCE; 2100.101.01
FILTE REFERENCE; 2000.09-18
FILTE REPRENCE; 2000.09-18
FILTE REPRENCE; 2000.09-18
FILTE REPRENCE; 2000.09-18
FILTE REPRENCE; 2000.09-18
FILTER PROPERTY TO NUMBER: 60/226,973
FRICE FILTEN DATE: 2000.09-18
FRICE FILTEN SHENER; 2000.09-18
FRICE FILTEN SHENER; 60/223,675
FRICE FILTEN SHENER; 2000.09-18
FRICE FILTEN SHENER; 2000.09-18
FRICE FILTEN SHENER; 2000.09-18
FRICE FILTEN SHENER; 2000.09-18
FRICE FILTEN SHENER; 2000.09-19
FRICE FILTEN SHENER;
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Conservative:
Mismatches:
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TCHERNEV, VELIZAR T
MALYANKAR, URIEL M.
SHENOY, SURESH
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ORGANISM: Unknown Organism
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Best Local Similarity:
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GREAT INFORMATION:

APPLICANT: Burgees, Catherine

APPLICANT: Gueev, Vladimir Y

APPLICANT: Majumder, Kumud

APPLICANT: Majumder, Kumud

APPLICANT: Majumder, Kumud

APPLICANT: Padigaru, Muralidhar

APPLICANT: Shimkets, Richard A

APPLICANT: Shimkets, Richard A

APPLICANT: Spaceria, Steven K

APPLICANT: Spaceria, Spaceria, Spaceria, Steven K

APPLICANT: Spaceria, S
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Matches:
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                                                                                                                Sequence 56, Application US/09823187
Publication No. US20030096952A1
GENERAL INFORMATION:
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67.48%
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Best Local Similarity:
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                                                                                                              206 ACTITICCTGTGGAACCTGCTGGTTCCGGTCACCATCCCGCGGGTCCGTGCCTTCCACCGC
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APPLICANT: Padigaru, Muralidhar
APPLICANT: Patturajan, Meera
APPLICANT: Shinkets, Richard A
APPLICANT: Spaderra, Steven K
APPLICANT: Spaderra, Steven K
APPLICANT: Spaderra, Steven K
APPLICANT: Spaderra, Steven K
APPLICANT: Taubier, Raymond J
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
CURRENT APPLICATION NUMBER: 06/193,339
RRIOR PAPLICATION NUMBER: 60/193,339
RRIOR PILING DATE: 2000-03-30
PRIOR PILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,088
PRIOR APPLICATION NUMBER: 60/195,088
PRIOR APPLICATION NUMBER: 60/195,088
PRIOR PELING DATE: 2000-04-06
PRIOR PELING DATE: 2000-04-06
PRIOR PELING DATE: 2000-04-10
PRIOR PELING DATE: 2000-04-10
PRIOR PELING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/196,556
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/197,081
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/197,525
PRIOR FILING DATE: 2000-04-14
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1453.50
83.38%
78.10%
67.48%
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Best Local Similarity:
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LENGIH: 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGGAGAGCGAGCAGCCATGATGGTGGAATTCTGATTGGCGTGTTTGTGCTGTGCTGG 964
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              244
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                                ACAGCTTTTAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAGA 1141
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                                                                                                                                                                                                                                                                                                                                                                                                                              545 GCGCTCGCCCGGGTGCCGTCGCCTCATCGCCCTCGCGCCGCTGCTCTTTGGCCGGGGC
                                                                                                   CTAGTGCTGCTGATGCCTGTTTCCTGTGGAACCTGCTGGTTCCGGTCACCATCCCG
                                                                                 CGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTCTCGGAC
                                                                                                                                                   GAACTAGTGGCAGCGCTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGA
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                                                                            65 ACCAGCAGCGGACCCCGAAGCCCGAGAGGGATACTCGGTTCGACCCCGAGGGC 124
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                                         CGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGGCCGTCTCGGAC
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US-09-976-782-15 (1-1152) x US-09-823-187-57 (1-370)
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Sequence 57, Application US/09823187 Publication No. US20030096952A1 GENERAL INFORMATION:

-09-823-187-57

APPLICANT: Burgess, Catherine APPLICANT: Gusev, Vladimir Y APPLICANT: Liu, Xiaohong APPLICANT: Majumder, Kumud

Mismatches: Indels:

Length: Matches: Conservative:

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65 ACCAGCAGCGGACCCGGGACCCCAAGCCCGAGAGGGATACTCGGTTCGACCCCGAGCGGC 124
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                                                                                   THEREBY
                                               | APPLICANT: ZERHUSEN, BRYNN
| TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THERE
| CURRENT FILLING DATE: 2001-09-17
| CURRENT FILLING DATE: 2001-09-17
| PRIOR APPLICATION NUMBER: 05/233,382
| PRIOR FILLING DATE: 2000-09-18
| PRIOR FILLING DATE: 2000-09-18
| PRIOR FILLING DATE: 2000-01-13
| PRIOR PLILING DATE: 2001-01-013
| PRIOR PAPLICATION NUMBER: 60/260,933
| PRIOR PAPLICATION NUMBER: 60/260,933
| PRIOR PAPLICATION NUMBER: 60/260,933
| PRIOR FILLING DATE: 2001-01-06
| PRIOR PAPLICATION NUMBER: 60/264,794
| PRIOR FILLING DATE: 2001-01-06
| PRIOR FILLING DATE: 2001-01-06
| PRIOR FILLING DATE: 2001-01-06
| PRIOR FILLING DATE: 2000-09-18
| PRIOR FILLING DATE: 2000-09-19
| PRIOR PILLING DATE: 2000-09-19
| PRIOR PAPLICATION NUMBER: 60/232,676
| PRIOR PAPLICATION NUMBER: 60/233,801
| PRIOR PILLING DATE: 2000-09-19
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Mismatches:
Indels:
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1453.50
83.38%
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                       LI, LI
RASTELLI, LUCA
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 56
LENGTH: 370
TYPE: PRT
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Query Match:
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|AlaIleThrTrpAlaLeuSerAlaLeuIleAlaLeuAlaProLeuLeuPheGlyTrpGly 195
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                                                         CTGTGCTGCCCCCCCCCCCCTCGGGAACGTGGCGCCATCGCCCTGGGCCGCGAACGGGCCC 484
                                                                                                                                                                                                                                                                                       GAGGTGTGCGACGCTCGGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCCTATGCCGCC 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGCCACATTGCAAAGCAACGCTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGGGAGCAG 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 ThralaargCysargalaThrValalaPheGlnThrSerGlyAspSerTrpArgGluGln 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1085 ACAGCTITIAACAAGAACTACAACAATGCCTTCAAGAGCCTCTTTACTAAGCAGAGA 1141
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                                                                               AAGGAGAGCGAGCACCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTGCTGC
                                                                                                                                  ATCACACGCCCCTGCAGCACACGCTGCGCACCCGCAGCCGCGCCTCGTTGCTCATGATC
                                                                                                                                                                                                                                                                                                                                                              TTCTCCACCCGCGCGCCTTCCACCTGCCGCTTGGCGTGCCGTTTGTCTACCGGAAG
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|-----ArgTrpGlnLeuGlyArgSerLeuCysHisValTrpIleSerPheAspVal
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Publication No. US20030170838A1
GENERAL INFORMATION:
APPLICANT: MISHRA, VISHNU S.
APPLICANT: SPYTEK, KIMBERLY ANN
APPLICANT: VENDET, CORINE A.
APPLICANT: VENDET, CORINE A.
APPLICANT: COLMAN, STEVEN D.
APPLICANT: GOLMAN, STEVEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCHERNEY, VELIZAR T.
MALYANKAR, VELIZAR T.
SHENOY, SURESH
PADIGARU, MURALIDHARA
GERLACH, VALERIE I.
MACDOUGALL, JOHN R.
SMITHSON, GLENNDA
MILLET, ISABELLE
BEYMAN, JOHN
STONE, DAVID
GUNTHER, BRIK
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PRIOR APPLICATION NUMBER: 60/240,732
PRIOR FILING DATE: 2000-10-16
PRIOR PAPLICATION NUMBER: 60/240,625
PRIOR PAPLICATION NUMBER: 60/240,703
PRIOR PILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/241,190
PRIOR PILING DATE: 2000-10-16
PRIOR PELING DATE: 2000-10-16
PRIOR PELING DATE: 2000-10-16
PRIOR PRILING DATE: 2000-10-16
PRIOR FILING DATE: 2000-10-18
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2000-10-16
NUMBER: 0F SEQ ID NOS: 127
SOFFWARE: PALENTIN VONER: 60/240,648
PRIOR FILING DATE: 2000-10-16
NUMBER: 0F SEQ ID NOS: 127
FEMALE PALENTING DATE: 2000-10-16
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Publication No. US20030190715A1
GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GEOSSS et al

TITLE OF INVENTION: No. US20030190715A1e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-157
CURRENT APPLICATION NUMBER: US/09/976,782
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,113
PRIOR PILING DATE: 2000-110-12
PRIOR PAPLICATION NUMBER: 60/240,662
PRIOR PILING DATE: 2000-10-16
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Conservative:
Mismatches:
Indels:
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               GAGGTGTGCGACGCTCGGCTCCAGCGCTGCCAGGTGAGCCGGGAACCCTCTATGCCGCC 664
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APPLICANT: Spaderna, Steven K
APPLICANT: Spaderna, Spacer, Kimberly
APPLICANT: Taupier, Raymond J
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
CURRENT APPLICATION NUMBER: US/09/93,187
CURRENT APPLICATION NUMBER: US/01/93,339
PRIOR APPLICATION NUMBER: 60/193,205
PRIOR PILING DATE: 2000-03-30
PRIOR PILING DATE: 2000-04-05
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,005
PRIOR PILING DATE: 2000-04-10
PRIOR PILING DATE: 2000-04-10
PRIOR PILING DATE: 2000-04-10
PRIOR PILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/195,005
PRIOR PILING DATE: 2000-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 58, Application US/09823187; Publication No. US20030096952A1
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine
APPLICANT: Liu, Xiaohong
APPLICANT: Majumder, Kumud
APPLICANT: Padigaru, Muralidhar
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US-09-823-187-58
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APPLICANT:
APPLICANT:
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ORGANISM: Mus musculus
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: RASTELLI, LUCA
APPLICANT: ZERHUSEN, BRYAN
ITTLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 21402-114
CURRENT APPLICATION NUMBER: US/09/954,342
CURRENT PILING DATE: 2001-09-18
FRIOR FILING DATE: 2000-09-18
FRIOR FILING DATE: 2000-10-13
FRIOR FILING DATE: 2000-10-13
FRIOR FILING DATE: 2000-10-13
FRIOR FILING DATE: 2000-10-13
FRIOR FILING DATE: 2001-01-08
FRIOR PELICATION NUMBER: 60/260,973
FRIOR APPLICATION NUMBER: 60/260,973
FRIOR APPLICATION NUMBER: 60/264,794
FRIOR APPLICATION NUMBER: 60/24,794
FRIOR APPLICATION NUMBER: 60/232,675
FRIOR APPLICATION NUMBER: 60/232,675
FRIOR PELING DATE: 2000-09-15
FRIOR PELING DATE: 2000-09-15
FRIOR PELING DATE: 2000-09-15
FRIOR APPLICATION NUMBER: 60/232,675
FRIOR APPLICATION NUMBER: 60/233,801
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                      AAGGAGAGCGAGCCATGATGGTGGGAATTCTGATTGGCGTGTTTGTGCTGTGTGCTGG 964
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APPLICANT: MISHRA, VISHNU S.
APPLICANT: TAUPIER, KIMBERLY ANN
APPLICANT: TAUPIER, RAYMOND J.
APPLICANT: COLMAN, STEVEN D.
APPLICANT: COLMAN, STEVEN D.
APPLICANT: COLMAN, LINDA
APPLICANT: TCHERNEY, VELIZAR T.
APPLICANT: SHENOY, VELIZAR T.
APPLICANT: SHENOY, VELIZER T.
APPLICANT: GERLACH, WIRELIDHARA
APPLICANT: SHENOY, SURESH
APPLICANT: SHILEY, VALERIE L.
APPLICANT: SMITHSON, GLENNDA
APPLICANT: SMITHSON, GLENNDA
APPLICANT: STONE, DAVID
APPLICANT: STONE, DAVID
APPLICANT: ELLERMAN, KAREN
APPLICANT: ELLERMAN, KAREN
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Publication No. US20030170838Al
GENERAL INFORMATION:
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RASTELLI, LUCA
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| ArgTrpGlnLeuGlyArgSerLeuCysHisValTrpIleSerPheAspVal----
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Mismatches:
Indels:
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Matches:
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/233,960
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 60/233,402
PRIOR FILING DATE: 2000-00-18
PRIOR PRILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-15
SOFTWARRE: PATCHING DATE: 2000-09-15
SOFTWARRE: PATCHING DATE: 2000-09-15
LENGTH: 370
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1452.50
83.64%
78.63%
67.43%
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Percent Similarity: 83.64\$ Conservative: 19 Best Local Similarity: 78.63\$ Mismatches: 53 Query Match: 67.43\$ Indels: 9 DB: 10 Gaps: 3 US-09-976-782-15 (1-1152) x US-09-976-782-102 (1-370)	<pre>Qy 5 AIGGAGGCGCTAGCCTTTCAGTGGCCACCGCGGGGTTGCCCTTGCCCTGGGACCCGAG 64 </pre>	Oy 65 ACCAGCAGCGGACCCCAAGCCCGAGGGATACTCGGTTCGACCCCGAGCGC 124 :::	OY 125 GCGTCCTGCCGGGCCGGGCCGCCTTCTCTGTCTTCACGGTCCTGGTGACGCTG 184 :::	OY 185 CTAGTGCTGCTGCTGCACTTTCCTGTGGAACCTGCTGGTCGCTCACCATCCG 244	Oy 245 CGGGTCCGTGCCTTCCACCGCGTGCCGCATAACTTGGTGGCCTCGACGCCGTCTCGGAC 304	Oy 305 GAACTAGTGGCGCGTGGCGATGCCACCGAGCCTGGCGAGTGAGCTGTCGACCGGGCGA 364	Qy 365 CGTCGCTGGCCCGGAGCCTGTGCCACGTGTGGATCTCCTTCGACGCCGGAGCCTGT 424	Qy 425 CTGTGCTGCCGCGGCGTGGGGAACGTGGCGATCGCCCTGGGCGGCGACGGGGCC 484	Oy 485 AICACACGCACCTGCAGCACACGCTGCGCACCCGCAGCCGCGCCTCGTTGCTCATGATC 544	Oy 545 GCGCTCGCCGGGTGCCGTCGGCGCTCATCGCCCCTCGCCCGCTGCTCTTTGGCCGGGGC 604	QY 605 GAGGTGCGACGCTCCAGGGCTGCCAGGTGAGCCGGAACCCTCTATGCCGCC 664	Qy 665 TTCTCCACCGCGGCGCCTTCCACCTGCCGCTTGGCGTGCCGTTTGTCTACCGGAAG 724	Oy 725 ATCTACGAGGCCCAAGTTTCGTTTCGGCCGCCGCGGGAGAGCTGTGCTGCCGTTGCCG 784	OY 785 GCCACCATGCAGGTGCAAGGTAAAGGAAGCACCTGATGAGGTGGTGTTC 844	OY 845 ACGGCACATTGCAAAGGATGTCCTTCCAGGTGAGGGGGACTCCTGGGGGAGCAG 904	Qy 905 AAGGAGAGCAGCCATGATGATGGGAATTCTGATTGGCGTGTTTGTGCTGG 964	965 ATCCCTTCTTCCTGACGGAACTCATCAGCCCACTCTGTGCCTGCAGCCTGCCCCCATC
Qy 665 TTCTCCACCCGCGGGCGCTTCCACCTGCCGCTTGGCGTTTGTCTACCGGAAG 724 Db 216 PheSerThrCysGlyAlaPheTyrLeuProLeuAlaValValLeuPheValTyrTrpLys 235 Qy 725 ATCTACGAGGCGCCAAGTTTCGTTTCGGCCGCCGCCGGCGGGGGGTGTGCCGTTGCCGTTGCCGTTGCCGTTGCCGTTGCCGTTGCCGTTGCCGTTGCCGTTGCCGTTGCTGC	785 GCCACCATGCAGGTCCAAGGTAAAGAAAGAACGACCTGATGAGGTGTAAGGTGTGTTC 84 256 AlalhithtGland	ACGGCACATIGCAAAGCAACGGTGTCCTTCCAGGTGAGCGGGGACTCCTGGCGGGGACAG	CTGG 9 sTrp 3	QY 965 ATCCCTTCTTCCTGACGGAACTCATCAGCCCACTCTGTGCCTGCC	TTAC 	A 114 370		; Publication No. US20030190715A1 ; GENERAL INFORMATION: ; APPLICANT: Grosse et al. 1320030190715A1e1 Profeins and Nucleic Acids Proceding Came		PRIOR FILING DATE: 2000-10-12 PRIOR APPLICATION NUMBER: 60/240,662 PRIOR PILING DATE: 2000-10-16 PRIOR APPLICATION NUMBER: 60/240,322	PRIOR FILING DATE: 2000-10-16 PRIOR APPLICATION NUMBER: 60/240,625 PRIOR FILING DATE: 2000-10-16 PRIOR APPLICATION NUMBER: 60/240 703	PRIOR FILING DATE: 2000-10-16 PRIOR APPLICATION NUMBER: 60/241,190 PRIOR APPLICATION NUMBER: 60/241,200-10-16 PRIOR APPLICATION NUMBER: 60/240,237	PRIOR FILING DATE: 2000-10-16 PRIOR APPLICATION NUMBER: 60/240,669 PRIOR APPLICATION NUMBER: 60/240,669 PRIOR APPLICATION NUMBER: 60/240,465 PRIOR APPLICATION NUMBER: 60/262 455	PRIOR FILING DATE: 2001-01-19 PRIOR APPLICATION NUMBER: 60/240,648 PRIOR APPLICATION TO BOTE: 2000-10-16 NUMBER OF SECTION 127	SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 102 ; LENGTH: 370 ; TYPE: PRT	; ORGANISM: Mus musculus US-09-976-782-102	Alignment Scores: Pred. No.: 4.66e-82 Length: 370 Score: 1452.50 Matches: 298

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| AlaileThrTrpAlaLeuSerAlaLeuIleAlaLeuAlaProLeuLeuPheGlyTrpGly 195
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Liu, Xiachong
APPLICANT: Majumder; Kumud
, APPLICANT: Padigaru, Muralidhar
) APPLICANT: Padigaru, Muralidhar
) APPLICANT: Shimkets, Richard A
APPLICANT: Spaderna, Steven K
) APPLICANT: Spytek, Kimberly
APPLICANT: Spytek, Kimberly
APPLICANT: Spytek, Kimberly
APPLICANT: Spytek, Kimberly
APPLICANT: L996-745
CURRENT FILING DATE: 2001-03-29
PRIOR PELING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/193,205
PRIOR PLING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
PRIOR PLING DATE: 2000-03-30
PRIOR PLING DATE: 2000-03-30
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                                              ThralaPheAsnIysAsnIyrAsnAsnAlaPheLysSerLeuPheThrLysGlnArg
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publication No. US20030009780A1

GENERAL INPORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING 5-HT5B

TITLE OF INVENTION: SEROTONIN RECEPTOR GENE DISRUPTIONS
FILE REPERENCE: R-601

CURRENT APPLICATION NUMBER: US/10/109,532A

CURRENT FILING DATE: 2002-03-28

PRIOR PILING DATE: 2003-03

PRIOR PLING DATE: 2001-03-29

PRIOR FILING DATE: 2001-13-29

PRIOR FILING DATE: 2001-12-21
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity:
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Pred. No.:
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Mismatches:
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Matches:
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PRIOR APPLICATION NUMBER: 60/195,005
PRIOR FILING DATE: 2000-04-06
PRIOR PPLICATION NUMBER: 60/195,792
PRIOR APPLICATION NUMBER: 60/196,556
PRIOR APPLICATION NUMBER: 60/196,556
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PATCHTIN VET: 2.1
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83.38%
78.10%
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ORGANISM: Rattus norvegicus
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Percent Similarity:
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US-09-823-187-59
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TTCTCCACCCGCGCGCCTTCCACCTGCCGCTTGGCGTGCCGTTTGTCTACCGGAAG
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Search completed: August 31, 2004, 20:46:12 Job time : 184 secs